OM protein - protein search, using sw model
Run on: September 19, 2007, 18:43:42 ; Search time 215 Seconds
                                             (without alignments)
                                     980.943 Million cell updates/sec

Title: US-10-677-471-83
Perfect score: 2211
Sequence: 1 MFFGGEGSLTYTVIICFLT.........LRRKRYSRLDYLINGIYVDI 431
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 2782304 seqs, 48933398 residues
Total number of hits satisfying chosen parameters: 2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :   A_Geneseq_200701:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 11: geneseqp2007s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
                                 SUMMARIES

No.   Score   Match   Length DB   ID   Description

RESULT 1
ID   AAY17834 standard; protein; 431 AA.
DE   Human PRO361 protein sequence.
PN   WO9928462-A2.
PD   10-JUN-1999.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 2; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 2
ID   AAB33428 standard; protein; 431 AA.
DE   Human PRO361 protein UNQ316 SEQ ID NO:72.
PN   WO200053758-A2.
PD   14-SEP-2000.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 3; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 3
ID   AAB01325 standard; protein; 431 AA.
DE   Human PRO361 polypeptide.
PN   WO200032776-A2.
PD   08-JUN-2000.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 3; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 4
ID   AAB34739 standard; protein; 431 AA.
DE   Human secreted protein encoded by DNA clone vo27 1.
PN   WO200055375-A1.
PD   21-SEP-2000.
PA   (ALPH-) ALPHAGENE INC.
        Query Match   100.0%;   Score 2211; DB 3; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 5
ID   AAB95464 standard; protein; 431 AA.
DB   Human protein sequence SEQ ID NO:17950.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST
        Query Match   100.0%;   Score 2211; DB 4; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 6
ID   AAB65299 standard; protein; 431 AA.

DE   Human PRO361 protein sequence SEQ ID NO:515.
PN   WO20073454-A1.
PD   07-DEC-2000.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 4; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 7
ID   ABU55934 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2002142959-A1.
PD   03-OCT-2002.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 8
ID   ABU58114 standard; protein; 431 AA.
DE   Human PRO polypeptide #146.
PN   US2003027163-A1.
PD   06-FEB-2003.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 9
ID   ABU59192 standard; protein; 431 AA.
DE   Novel human secreted or transmembrane protein PRO361.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 10
ID   ABU82704 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003032023-A1.
PD   13-FEB-2003.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 11
ID   ABU60623 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein, #182.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 12
ID   ABU14005 standard; protein; 431 AA.
DE   Human PRO361 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH) GENENTECH LTD.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 13
ID   ABU60244 standard; protein; 431 AA.
DE   Human PRO polypeptide #15.
PN   US2002213768-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 14
ID   ABU72590 standard; protein; 431 AA.
DE   Novel human secreted and transmembrane protein PRO361.
PN   US2003003531-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
        Query Match   100.0%;   Score 2211; DB 6; Length 431;
        Best Local Similarity 100.0%;   Pred. No. 6.4e-173;

RESULT 15
ID   ABU64930 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2002173463-A1.
PD   21-NOV-2002.

PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 16
ID ABU58364 standard; protein; 431 AA.
DE Novel human secreted protein PRO361.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 17
ID ABU57250 standard; protein; 431 AA.
DE Human PRO361 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 18
ID ABU59939 standard; protein; 431 AA.
DE Human secreted/transmembrane protein, #182.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 19
ID ABO26036 standard; protein; 431 AA.
DE Human PRO361 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 20
ID ABU56315 standard; protein; 431 AA.
DE Human secreted/transmembrane protein, PRO361.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 21
ID ABU60355 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 22
ID ABU59045 standard; protein; 431 AA.
DE Human sectreted/transmembrane protein, #182.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 23
ID ABU92423 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 24
ID ABU59488 standard; protein; 431 AA.
DE Novel human secreted or transmembrane protein PRO846.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 25

ID ABU92254 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003017476-A1.
PD 23-JAN-2003.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 26
ID ABU10960 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 27
ID ABU11316 standard; protein; 431 AA.
DE Human pro361 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 28
ID ABU67135 standard; protein; 431 AA.
DE Human PRO polypeptide #15.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 29
ID ABU81712 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 30
ID ABU88651 standard; protein; 431 AA.
DE Human secreted and transmembrane polypeptide PRO361.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 31
ID ABO34165 standard; protein; 431 AA.
DE Human PRO361 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 32
ID ADA38026 standard; protein; 431 AA.
DE Human secreted/transmembrane protein PRO361.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 33
ID ADA21712 standard; protein; 431 AA.
DE Human secreted/transmembrane polypeptide PRO361.
PN US2003054404-A1.
PD 20-MAR-2003.
    Query Match   100.0%; Score 2211; DB 6; Length 431;
    Best Local Similarity 100.0%; Pred. No. 6.4e-173;
RESULT 34
ID ADA10499 standard; protein; 431 AA.
DE Human secreted/transmembrane protein, PRO361.
PN US2003059831-A1.
PD 27-MAR-2003.

ID   ADA18043 standard; protein; 431 AA.
DE   Human PRO361 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
Query Match   100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 35
ID   ADA28151 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003054359-A1.
PD   20-MAR-2003.
Query Match   100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 36
ID   ADA94731 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003059832-A1.
PD   27-MAR-2003.
Query Match   100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 37
ID   ADA38956 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003059780-A1.
PD   27-MAR-2003.
Query Match   100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 38
ID   ADA93077 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003060407-A1.
PD   27-MAR-2003.
Query Match   100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 39
ID   AB053251 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003044806-A1.
PD   06-MAR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 40
ID   ADA22638 standard; protein; 431 AA.
DE   Human secreted/transmembrane polypeptide PRO361.
PN   US2003040473-A1.
PD   27-FEB-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 41
ID   AB022621 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003017982-A1.
PD   23-JAN-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 42
ID   ADA06804 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #146.
PN   US2003049638-A1.
PD   13-MAR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 43
ID   ADA39497 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003059782-A1.
PD   27-MAR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 44

ID   ADB96523 standard; protein; 431 AA.
DE   Human PRO polypeptide #146.
PN   US2003054403-A1.
PD   20-MAR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 46
ID   ADC57995 standard; protein; 431 AA.
DE   Human PRO polypeptide #146.
PN   US2003027754-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 47
ID   ADC25839 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2002142419-A1.
PD   03-OCT-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 48
ID   ADC25597 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2002156004-A1.
PD   24-OCT-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 49
ID   ADC55359 standard; protein; 431 AA.
DE   Human PRO polypeptide #146.
PN   US2003045463-A1.
PD   06-MAR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 50
ID   ADC12226 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003049681-A1.
PD   13-MAR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 51
ID   ADC56648 standard; protein; 431 AA.
DE   Human PRO polypeptide #146.
PN   US2003064375-A1.
PD   03-APR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 52
ID   ADC11693 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003069403-A1.
PD   10-APR-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 53
ID   ADC25718 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2003077698-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 54
ID   ADC14815 standard; protein; 431 AA.
DE   Novel human secreted and transmembrane protein PRO361.
PN   US2003082546-A1.
PD   01-MAY-2003.
Query Match   100.0%; Score 2211; DB 7; Length 431;
Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 55

ID ADD08347 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003068623-A1.
PD 10-APR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 56
ID ADC82172 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2003083461-A1.
PD 01-MAY-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 57
ID ADD07814 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 58
ID ADC82705 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2003059833-A1.
PD 27-MAR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 59
ID ADD08885 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003073090-A1.
PD 17-APR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 60
ID ADD07134 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 61
ID ADC83381 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2003059783-A1.
PD 27-MAR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 62
ID ADD55488 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2003077593-A1.
PD 24-APR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 63
ID ADD56446 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2003077594-A1.
PD 24-APR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 64
ID ADD54884 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 65

ID ADE31903 standard; protein; 431 AA.
DE Human secreted/transmembrane protein PRO361.
PN US2003066647-A1.
PD 10-APR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 66
ID ADC27038 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003087304-A1.
PD 08-MAY-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 67
ID ADE26505 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003087305-A1.
PD 08-MAY-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 68
ID ADF67442 standard; protein; 431 AA.
DE Human PRO361 amino acid sequence SEQ ID NO:515.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 69
ID ADH27503 standard; protein; 431 AA.
DE Human secreted/transmembrane PRO polypeptide #15.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 70
ID ADI35696 standard; protein; 431 AA.
DE Human PRO polypeptide #146.
PN US2003050457-A1.
PD 13-MAR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 71
ID ADI00189 standard; protein; 431 AA.
DE Novel human secreted and transmembrane protein PRO361.
PN US2003049682-A1.
PD 13-MAR-2003.
    Query Match   100.0%; Score 2211; DB 7; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 72
ID ADE71552 standard; protein; 431 AA.
DE Human secreted/transmembrane PRO polypeptide #15.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 8; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 73
ID ADF35641 standard; protein; 431 AA.
DE Human PRO361 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
    Query Match   100.0%; Score 2211; DB 8; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;
RESULT 74
ID ADG11891 standard; protein; 431 AA.
DE Human PRO361 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 2211; DB 8; Length 431;
    Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 75
ID   ADG63495 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2003211570-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 76
ID   ADH19761 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 77
ID   ADH21254 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003224358-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 78
ID   ADH20294 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein PRO361.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 79
ID   ADH43224 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2003207401-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 80
ID   ADN00462 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2004091972-A1.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 81
ID   ADU25386 standard; protein; 431 AA.
DE   Human secreted/transmembrane PRO polypeptide #15.
PN   US2004220385-A1.
PD   04-NOV-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 8; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 82
ID   ADY39549 standard; protein; 431 AA.
DE   Human mucin/chitinase homolog PRO361 precursor protein.
PN   US2005048613-A1.
PD   03-MAR-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 9; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 83
ID   ADY73830 standard; protein; 431 AA.
DE   Human PRO361 protein, SEQ ID NO: 83.
PN   US2005059115-A1.
PD   17-MAR-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 9; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 84
ID   ABA38663 standard; protein; 431 AA.
DE   Human secreted/transmembrane protein, #214.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 9; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 85
ID   AEH50179 standard; protein; 431 AA.
DE   Human cDNA clone DNA45410-1250 protein product PRO361 SEQ ID NO: 83.
PN   US2006105427-A1.
PD   18-MAY-2006.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 10; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 86
ID   ABI36387 standard; protein; 431 AA.
DE   Human PRO protein amino acid sequence - SEQ ID 83.
PN   US2006127983-A1.
PD   15-JUN-2006.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 2211; DB 10; Length 431;
  Best Local Similarity   100.0%; Pred. No. 6.4e-173;

RESULT 87
ID   AAB92667 standard; protein; 397 AA.
DE   Human protein sequence SEQ ID NO:11028.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
Query Match   91.5%; Score 2022; DB 4; Length 397;
  Best Local Similarity   92.1%; Pred. No. 2e-157;

RESULT 88
ID   ADJ75679 standard; protein; 397 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:931.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
Query Match   91.5%; Score 2022; DB 8; Length 397;
  Best Local Similarity   92.1%; Pred. No. 2e-157;

RESULT 89
ID   ADN05896 standard; protein; 397 AA.
DE   Antipsoriatic protein sequence #1111.
PN   WO2004028479-A2.
PD   08-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   91.5%; Score 2022; DB 8; Length 397;
  Best Local Similarity   92.1%; Pred. No. 2e-157;

RESULT 90
ID   AAM25899 standard; protein; 365 AA.
DE   Human protein sequence SEQ ID NO:1414.
PN   WO200153455-A2.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   84.9%; Score 1877; DB 4; Length 365;
  Best Local Similarity   100.0%; Pred. No. 1.5e-145;

RESULT 91
ID   AAY94917 standard; protein; 300 AA.
DE   Human secreted protein clone cf85_1 protein sequence SEQ ID NO:40.
PN   WO200009552-A1.
PD   24-FEB-2000.
PA   (GEMY) GENETICS INST INC.
Query Match   66.9%; Score 1479; DB 3; Length 300;
  Best Local Similarity   99.7%; Pred. No. 6.5e-113;

RESULT 92
ID   ADJ76374 standard; protein; 414 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1626.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (GENO-) GENOX RES INC.
Query Match   52.7%; Score 1164.5; DB 8; Length 414;
  Best Local Similarity   59.9%; Pred. No. 7.8e-87;

RESULT 93
ID   ABB89239 standard; protein; 218 AA.
DE   Human polypeptide SEQ ID NO 1615.

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PN   WO20190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match    45.0%;  Score 994;  DB 5;  Length 218;
     Best Local Similarity    91.7%;  Pred. No. 3.3e-73;
RESULT 94
ID   AAB42382 standard; protein; 172 AA.
DE   Human ORFX ORF2146 polypeptide sequence SEQ ID NO:4292.
PN   WO20058473-A2.
PD   05-OCT-2000.
PA   (CURA-) CURAGEN CORP.
     Query Match    39.1%;  Score 865;  DB 3;  Length 172;
     Best Local Similarity    99.4%;  Pred. No. 9.8e-63;
RESULT 95
ID   ADP29428 standard; protein; 47 AA.
DE   Human secreted protein SEQ ID #1426.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
     Query Match    11.8%;  Score 261;  DB 8;  Length 47;
     Best Local Similarity   100.0%;  Pred. No. 7.7e-14;
RESULT 96
ID   ADL91883 standard; protein; 449 AA.
DE   Human PRO60929 protein SEQ ID NO:104.
PN   WO2004024076-A2.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match     8.9%;  Score 197;  DB 8;  Length 449;
     Best Local Similarity    22.2%;  Pred. No. 3.5e-07;
RESULT 97
ID   AAE21468 standard; protein; 342 AA.
DE   Human gene 17 encoded secreted protein HLDQZ72, SEQ ID NO:84.
PN   WO200224719-A1.
PD   28-MAR-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     8.9%;  Score 196.5;  DB 5;  Length 342;
     Best Local Similarity    24.4%;  Pred. No. 2.6e-07;
RESULT 98
ID   ABG64986 standard; protein; 342 AA.
DE   Human albumin fusion protein #1661.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     8.9%;  Score 196.5;  DB 5;  Length 342;
     Best Local Similarity    24.4%;  Pred. No. 2.6e-07;
RESULT 99
ID   ADL78253 standard; protein; 342 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1735.
PN   US2004010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
     Query Match     8.9%;  Score 196.5;  DB 8;  Length 342;
     Best Local Similarity    24.4%;  Pred. No. 2.6e-07;
RESULT 100
ID   AEH08526 standard; protein; 342 AA.
DE   Therapeutic protein HLDQZ72, SEQ ID 1735.
PN   US2006084794-A1.
PD   20-APR-2006.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match     8.9%;  Score 196.5;  DB 10;  Length 342;
     Best Local Similarity    24.4%;  Pred. No. 2.6e-07;
RESULT 101
ID   AAB18965 standard; protein; 417 AA.
DE   Amino acid sequence of a human transmembrane protein.
PN   WO200056891-A2.
PD   28-SEP-2000.
PA   (INCY-) INCYTE PHARM INC.
     Query Match     8.8%;  Score 195.5;  DB 3;  Length 417;
     Best Local Similarity    23.4%;  Pred. No. 4.2e-07;
RESULT 102
ID   AAU12283 standard; protein; 449 AA.
DE   Human PRO4315 polypeptide sequence.


PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 4;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 103
ID   ABO17727 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US200303156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 104
ID   ABU80981 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 105
ID   ABU66681 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 106
ID   ABU59762 standard; protein; 449 AA.
DE   Novel secreted and transmembrane protein PRO4315.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 107
ID   ABO24952 standard; protein; 449 AA.
DE   Human secreted/transmembrane protein (PRO) #112.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 108
ID   ABU66957 standard; protein; 449 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 224.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 109
ID   ADA45743 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 110
ID   ADA76174 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     8.5%;  Score 188;  DB 6;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 111
ID   ADA18824 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003054517-A1.
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PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 112
ID   ADA61447 standard; protein; 449 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 113
ID   ADB19232 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 114
ID   ADB27773 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 115
ID   ADA86252 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 116
ID   ADB15816 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 117
ID   ADA47602 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 118
ID   ADA67397 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 119
ID   ADB30404 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 120
ID   ADA85700 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003082693-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 121
ID   ADA96912 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 122
ID   ADA79216 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 123
ID   ADA87355 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 124
ID   ADB16557 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 125
ID   ADA91649 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 126
ID   ADB14712 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 127
ID   ADB18673 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 128
ID   ADA93888 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
          Query Match   8.5%;   Score 188;   DB 6;   Length 449;
          Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 129
ID   ADB19784 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

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Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 130
ID   ADB13096 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 131
ID   AB043260 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 132
ID   ADA74350 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 133
ID   ADB24583 standard; protein; 449 AA.
DE   Human PRO polypeptide SEQ ID NO 224.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 134
ID   ADB82107 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 135
ID   ADA75070 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 136
ID   ADA85148 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 137
ID   ADA84596 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 138
ID   ADB29852 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 139
ID   ADA80380 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 140
ID   ADA75622 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 141
ID   ADA46847 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 142
ID   ADB25143 standard; protein; 449 AA.
DE   Human PRO polypeptide SEQ ID NO 224.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 143
ID   ADA93319 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 144
ID   ADB26669 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 145
ID   ADB30956 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 146
ID   ADA60884 standard; protein; 449 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 147
ID   ADA24031 standard; protein; 449 AA.
DE   Human PRO polypeptide SEQ ID NO 224.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          8.5%;   Score 188; DB 6; Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
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RESULT 148
ID ADA96360 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 6; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 149
ID ADA80932 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 6; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 150
ID ADA95808 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 6; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 151
ID ADB26117 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 6; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 152
ID ADB21602 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 6; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 153
ID ADA77381 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 154
ID ADB18121 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 155
ID ADA86804 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 156
ID ADA87907 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 157
ID ADA46295 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 158
ID ADB28325 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 159
ID ADB28877 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 160
ID ADA76829 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 161
ID ADA88459 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 162
ID ADA97464 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 163
ID ADB27221 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 164
ID ADB22154 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 165
ID ADA66845 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 8.5%; Score 188; DB 7; Length 449;
  Best Local Similarity 22.0%; Pred. No. 1.9e-06;
RESULT 166
ID ADB22706 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003077711-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 167
ID ADB23479 standard; protein; 449 AA.
DE Human PRO polypeptide SEQ ID NO 224.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 168
ID ADA92201 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 169
ID ADB15264 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 170
ID ADB38516 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 171
ID ADB37964 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003077347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 172
ID ADB66436 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 173
ID ADB89516 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 174
ID ADB90248 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 175
ID ADB39349 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082764-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 176
ID ADB46972 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 177
ID ADB65579 standard; protein; 449 AA.
DE Human PRO polypeptide #112.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 178
ID ADB77184 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 179
ID ADB34341 standard; protein; 449 AA.
DE Human PRO polypeptide SEQ ID NO 224.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 180
ID ADB35445 standard; protein; 449 AA.
DE Human PRO polypeptide SEQ ID NO 224.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 181
ID ADB33789 standard; protein; 449 AA.
DE Human PRO polypeptide SEQ ID NO 224.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 182
ID ADB34893 standard; protein; 449 AA.
DE Human PRO polypeptide SEQ ID NO 224.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 183
ID ADB35997 standard; protein; 449 AA.
DE Human PRO polypeptide SEQ ID NO 224.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   8.5%;   Score 188; DB 7; Length 449;
    Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 184
ID ADB46392 standard; protein; 449 AA.
DE Novel human secreted and transmembrane protein PRO4315.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 185
ID  ADC50265 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003092106-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 186
ID  ADC71812 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003092107-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 187
ID  ADC59791 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003092105-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 188
ID  ADC52798 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein Seq ID224.
PN  US2003087365-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 189
ID  ADC57152 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003087366-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 190
ID  ADC60343 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003087367-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 191
ID  ADC50818 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003087362-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 192
ID  ADC65345 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003087363-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 193
ID  ADC54443 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein Seq ID224.
PN  US2003087363-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 194
ID  ADC53404 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein Seq ID224.
PN  US2003087364-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 195
ID  ADC58927 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein Seq ID224.
PN  US2003087359-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 196
ID  ADC55805 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein Seq ID224.
PN  US2003087360-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 197
ID  ADC58375 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein Seq ID224.
PN  US2003087346-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 198
ID  ADD03049 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003092104-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 199
ID  ADC90041 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003087348-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 200
ID  ADC69460 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003194770-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 201
ID  ADC48349 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003194773-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 202
ID  ADD09878 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003194776-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
   Query Match            8.5%;   Score 188;  DB 7;  Length 449;
   Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
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RESULT 203
ID   ADD04453 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 204
ID   ADC80409 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 205
ID   ADD10916 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 206
ID   ADC47797 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 207
ID   ADC79857 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 208
ID   ADD09326 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 209
ID   ADD41039 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 210
ID   ADD52178 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 211
ID   ADD52918 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 212
ID   ADD53470 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 213
ID   ADD51626 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 214
ID   ADD02425 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 215
ID   ADD01859 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 216
ID   ADD54041 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 217
ID   ADD92358 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 218
ID   ADD91254 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 219
ID   ADE03868 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 220
ID   ADE32165 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   8.5%;
  Best Local Similarity   22.0%;   Score 188; DB 7; Length 449;
  Pred. No. 1.9e-06;
RESULT 221
ID   ADE22097 standard; protein; 449 AA.

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DE   Human PRO polypeptide #112.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 222
ID   ADD79321 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 223
ID   ADE41857 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 224
ID   ADE17674 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 225
ID   ADD91806 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 226
ID   ADE33269 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 227
ID   ADE33821 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 228
ID   ADD79873 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 229
ID   ADD92910 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 230
ID   ADE19330 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.

PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 231
ID   ADE18778 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 232
ID   ADE42974 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 233
ID   ADD95763 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 234
ID   ADE22649 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 235
ID   ADD78767 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 236
ID   ADE32717 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 237
ID   ADE42409 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 238
ID   ADD80425 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.          8.5%;   Score 188;  DB 7;   Length 449;
     Query Match                    22.0%;   Pred. No. 1.9e-06;
     Best Local Similarity
RESULT 239
ID   ADD89453 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199028-A1.
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PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 240
ID   ADE40737 standard; protein #112.
DE   Human PRO polypeptide #112.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 241
ID   ADE04536 standard; protein #112.
DE   Human PRO polypeptide #112.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 242
ID   ADE92665 standard; protein #112.
DE   Human PRO polypeptide #112.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 243
ID   ADG21374 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 244
ID   ADG23015 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 245
ID   ADF97350 standard; protein #112.
DE   Human PRO polypeptide #112.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 246
ID   ADG80414 standard; protein #112.
DE   Human PRO polypeptide #112.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 247
ID   ADG79862 standard; protein #112.
DE   Human PRO polypeptide #112.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 248
ID   ADH55154 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 249
ID   ADH55706 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 250
ID   ADI63925 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 251
ID   ADI64874 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 252
ID   ADI63373 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 253
ID   ADH81787 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 254
ID   ADH81235 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 255
ID   ADL25761 standard; protein; 449 AA.
DE   Human cancer suppressing protein #7.
PN   CN1403478-A.
PD   19-MAR-2003.
PA   (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 256
ID   ADM82404 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;  Score 188;  DB 7;  Length 449;
     Best Local Similarity   22.0%;
                             Pred. 449 AA.
RESULT 257
ID   ADN15803 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Query Match          8.5%;   Score 188; DB 7; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 258
ID   ADN16432 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 7; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 259
ID   ADN15251 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 7; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 260
ID   ADN14699 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 7; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 261
ID   ADC80961 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 262
ID   ADD76409 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 263
ID   ADD87773 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 264
ID   ADD86177 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 265
ID   ADE75625 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 266
ID   ADE23201 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;


Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 267
ID   ADE23753 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 268
ID   ADE24396 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 269
ID   ADD87221 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 270
ID   ADB89087 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 271
ID   ADB18226 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 272
ID   ADB88535 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 273
ID   ADB94555 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 274
ID   ADB90966 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 275
ID   ADB95107 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          8.5%;   Score 188; DB 8; Length 449;
Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
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RESULT 276
ID   ADE93217 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 277
ID   ADF34798 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 278
ID   ADE92113 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 279
ID   ADE90414 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 280
ID   ADE91561 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 281
ID   ADG02140 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 282
ID   ADG21926 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 283
ID   ADG19996 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 284
ID   ADF97902 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 285
ID   ADG24119 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 286
ID   ADF98473 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 287
ID   ADG03304 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 288
ID   ADF99025 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 289
ID   ADG16610 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 290
ID   ADG05069 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 291
ID   ADG19336 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 292
ID   ADG13173 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 293
ID   ADG08230 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             8.5%;
     Best Local Similarity   22.0%;
     Score 188; DB 8; Length 449;
     Pred. No. 1.9e-06;

RESULT 294
ID   ADG15400 standard; protein; 449 AA.
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DE   Human PRO polypeptide #112.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 295
ID   ADF96798 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 296
ID   ADG05983 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 297
ID   ADG23567 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 298
ID   ADG03856 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 299
ID   ADG24757 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 300
ID   ADG07054 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 301
ID   ADG07606 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 302
ID   ADG55101 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 303
ID   ADG60765 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.

PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 304
ID   ADG61869 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 305
ID   ADG82070 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 306
ID   ADG57309 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 307
ID   ADG56757 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 308
ID   ADG55653 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 309
ID   ADG58413 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 310
ID   ADG70779 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 311
ID   ADG57861 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       8.5%;  Score 188;  DB 8;  Length 449;
     Best Local Similarity    22.0%;  Pred. No. 1.9e-06;
RESULT 312
ID   ADG53445 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207415-A1.
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PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 313
ID  ADG71331 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207421-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 314
ID  ADH30480 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003077723-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 315
ID  ADH11847 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207419-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 316
ID  ADG52269 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207414-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 317
ID  ADG53997 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207416-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 318
ID  ADG80966 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003194793-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 319
ID  ADG56205 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207366-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 320
ID  ADH12471 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207378-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 321

    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 322
ID  ADG61317 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207429-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 323
ID  ADH28404 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003022331-A1.
PD  30-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 324
ID  ADG54549 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207367-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 325
ID  ADG59589 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207369-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 326
ID  ADI81013 standard; protein; 449 AA.
DE  Human PRO polypeptide #112.
PN  US2003207361-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 327
ID  ADG09756 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2004009548-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 328
ID  ADI15227 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207382-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 329
ID  ADG09104 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2004009547-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
    Best Local Similarity 22.0%;   Pred. No. 1.9e-06;
RESULT 330
ID  ADI14559 standard; protein; 449 AA.
DE  Novel human secreted and transmembrane protein PRO4315.
PN  US2003207383-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           8.5%;    Score 188;  DB 8;  Length 449;
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Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 331
ID   ADI18154 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 332
ID   ADJ63435 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 333
ID   ADJ77330 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 334
ID   ADJ65452 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 335
ID   ADM27588 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 336
ID   ADM42312 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 337
ID   ADM28174 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 338
ID   ADI95656 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 339
ID   ADI96208 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;

RESULT 340
ID   ADS32160 standard; protein; 449 AA.
DE   Novel human secreted and transmembrane protein PRO4315.
PN   US2004203125-A1.
PD   14-OCT-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 341
ID   ADT03144 standard; protein; 449 AA.
DE   Human PRO polypeptide #112.
PN   US2004214269-A1.
PD   28-OCT-2004.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 8;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 342
ID   ADZ03195 standard; protein; 449 AA.
DE   Human secreted/transmembrane PRO4315 protein.
PN   US2005074837-A1.
PD   07-APR-2005.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 9;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 343
ID   AEB13941 standard; protein; 449 AA.
DE   Cancer cell diagnosis method-related human protein - SEQ ID 224.
PN   US2005153396-A1.
PD   14-JUL-2005.
PA   (BAKE/) BAKER K P.
PA   (BERE/) BERESINI M.
PA   (DEFO/) DEFORGE L.
PA   (DESN/) DESNOYERS L.
PA   (FILV/) FILVAROFF E.
PA   (GAOW/) GAO W.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (SHER/) SHERWOOD S.
PA   (SMIT/) SMITH V.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
PA   (ZHAN/) ZHANG Z.
Query Match   8.5%;   Score 188; DB 9;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 344
ID   AED86139 standard; protein; 449 AA.
DE   Human PRO amino acid sequence, seq id 224.
PN   US2005245730-A1.
PD   03-NOV-2005.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 9;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 345
ID   AEG58086 standard; protein; 449 AA.
DE   Human PRO4315 polypeptide SEQ ID NO: 224.
PN   US2006073568-A1.
PD   06-APR-2006.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 188; DB 10;   Length 449;
Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 346
ID   AEI43731 standard; protein; 449 AA.
DE   Human cancer-related PRO protein amino acid sequence - SEQ ID 224.
PN   US2006040351-A1.
PD   23-FEB-2006.
PA   (BAKE/) BAKER K P.
PA   (BERE/) BERESINI M.
PA   (DEFO/) DEFORGE L.
PA   (DESN/) DESNOYERS L.

PA   (FILV/) FILVAROFF E.
PA   (GAOW/) GAO W.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (SHER/) SHERWOOD S.
PA   (SMIT/) SMITH V.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
PA   (ZHAN/) ZHANG Z.
      Query Match   8.5%;   Score 188; DB 10;   Length 449;
      Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 347
ID   AEI23814 standard; protein; 449 AA.
DE   Human secreted/transmembrane protein PRO4315, SEQ ID NO:224.
PN   EP1672070-A2.
PD   21-JUN-2006.
PA   (GETH) GENENTECH INC.
      Query Match   8.5%;   Score 188; DB 10;   Length 449;
      Best Local Similarity   22.0%;   Pred. No. 1.9e-06;
RESULT 348
ID   AAY91649 standard; protein; 266 AA.
DE   Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.
PN   WO20006698-A1.
PD   10-FEB-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   8.3%;   Score 183; DB 3;   Length 266;
      Best Local Similarity   27.2%;   Pred. No. 2.4e-06;
RESULT 349
ID   ADL71728 standard; protein; 266 AA.
DE   Novel human secreted protein fragment seqid 332.
PN   US2004034196-A1.
PD   19-FEB-2004.
PA   (KOMA/) KOMATSOULIS G A.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (DUAN/) DUAN D R.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (WEIY/) WEI Y.
      Query Match   8.3%;   Score 183; DB 8;   Length 2624;
      Best Local Similarity   27.2%;   Pred. No. 2.4e-06;
RESULT 350
ID   ADX97567 standard; protein; 2624 AA.
DE   Pancreatic cancer associated human protein, SEQ ID 115.
PN   EP1471075-A2.
PD   27-OCT-2004.
PA   (HINZ/) HINZMANN B.
PA   (ROSE/) ROSENTHAL A.
PA   (PILA/) PILARSKY C.
PA   (DAHL/) DAHL E.
PA   (SPEC/) SPECHT T.
PA   (LICH/) LICHTNER R.
      Query Match   7.8%;   Score 171.5; DB 8;   Length 2624;
      Best Local Similarity   22.4%;   Pred. No. 0.00054;
RESULT 351
ID   AEA08149 standard; protein; 4262 AA.
DE   Human mucin 17 (MUC17SEC) protein - SEQ ID 4.
PN   US2005100925-A1.
PD   12-MAY-2005.
PA   (BATR/) BATRA S.
PA   (MONI/) MONIAUX N.
      Query Match   7.4%;   Score 163; DB 9;   Length 4262;
      Best Local Similarity   22.7%;   Pred. No. 0.0054;
RESULT 352
ID   AEA08148 standard; protein; 4493 AA.
DE   Human mucin 17 protein - SEQ ID 3.
PN   US2005100925-A1.
PD   12-MAY-2005.

PA   (BATR/) BATRA S.
PA   (MONI/) MONIAUX N.
      Query Match   7.4%;   Score 163; DB 9;   Length 4493;
      Best Local Similarity   22.7%;   Pred. No. 0.0058;
RESULT 353
ID   AEB29721 standard; protein; 2448 AA.
DE   Human Mucin 5 (subtypes A and C).
PN   WO200506767-A2.
PD   28-JUL-2005.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
      Query Match   7.1%;   Score 157.5; DB 9;   Length 2448;
      Best Local Similarity   23.1%;   Pred. No. 0.0069;
RESULT 354
ID   ABP69313 standard; protein; 343 AA.
DE   Human polypeptide SEQ ID NO 1360.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSE-) HYSEQ INC.
      Query Match   7.1%;   Score 156.5; DB 5;   Length 343;
      Best Local Similarity   28.5%;   Pred. No. 0.00051;
RESULT 355
ID   AEB56507 standard; protein; 5858 AA.
DE   Radiochemotherapy response detection associated protein SEQ ID NO 82.
PN   WO200507341L-A1.
PD   11-AUG-2005.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
      Query Match   6.9%;   Score 153.5; DB 9;   Length 5858;
      Best Local Similarity   25.2%;   Pred. No. 0.051;
RESULT 356
ID   ADP84155 standard; protein; 22157 AA.
DE   Human CA125 protein sequence SeqID 5.
PN   WO200405553-A2.
PD   03-JUN-2004.
PA   (UYAR-) UNIV ARKANSAS.
      Query Match   6.9%;   Score 152.5; DB 8;   Length 22157;
      Best Local Similarity   23.2%;   Pred. No. 0.41;
RESULT 357
ID   ADR18920 standard; protein; 1225 AA.
DE   Human tracheobronchial mucin protein, MUC5A.
PN   WO200406136-A2.
PD   19-AUG-2004.
PA   (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
      Query Match   6.9%;   Score 151.5; DB 8;   Length 1225;
      Best Local Similarity   30.1%;   Pred. No. 0.0081;
RESULT 358
ID   AEI04881 standard; protein; 860 AA.
DE   Coccidioides posadasii strain C735 chitinase 2 (CTS2) protein.
PN   US2006121061-A1.
PD   08-JUN-2006.
PA   (UYOH-) UNIV OHIO MEDICAL.
      Query Match   6.8%;   Score 150.5; DB 10;   Length 860;
      Best Local Similarity   23.9%;   Pred. No. 0.0059;
RESULT 359
ID   ABU53163 standard; protein; 247 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #23.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
      Query Match   6.8%;   Score 149.5; DB 4;   Length 247;
      Best Local Similarity   34.1%;   Pred. No. 0.0012;
RESULT 360
ID   ABU53158 standard; protein; 260 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #18.
PN   WO20011265 9-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
      Query Match   6.8%;   Score 149.5; DB 4;   Length 260;
      Best Local Similarity   34.1%;   Pred. No. 0.0013;
RESULT 361
ID   ABU53162 standard; protein; 277 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #22.
PN   WO20011265 9-A2.
PD   22-FEB-2001.

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PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 277;
     Best Local Similarity   34.1%;  Pred. No. 0.0014;
RESULT 362
ID   ABU53157 standard; protein; 368 AA.
DE   Human testes-derived DKF2phtes3_2all homologue #17.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 368;
     Best Local Similarity   34.1%;  Pred. No. 0.0021;
RESULT 363
ID   ABU53156 standard; protein; 385 AA.
DE   Human testes-derived DKF2phtes3_2all homologue #16.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 385;
     Best Local Similarity   34.1%;  Pred. No. 0.0023;
RESULT 364
ID   ABU53159 standard; protein; 386 AA.
DE   Human testes-derived DKF2phtes3_2all homologue #19.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 386;
     Best Local Similarity   34.1%;  Pred. No. 0.0023;
RESULT 365
ID   ABU53161 standard; protein; 387 AA.
DE   Human testes-derived DKF2phtes3_2all homologue #21.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 387;
     Best Local Similarity   34.1%;  Pred. No. 0.0023;
RESULT 366
ID   ABU53160 standard; protein; 395 AA.
DE   Human testes-derived DKF2phtes3_2all homologue 20.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 395;
     Best Local Similarity   34.1%;  Pred. No. 0.0024;
RESULT 367
ID   ABU53144 standard; protein; 717 AA.
DE   Human testes-derived DKF2phtes3_2all homologue #4.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 717;
     Best Local Similarity   34.1%;  Pred. No. 0.0055;
RESULT 368
ID   ABP43908 standard; protein; 4315 AA.
DE   MUC5B partial gene protein.
PN   WO200231111-A2.
PD   18-APR-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match     6.8%;  Score 149.5; DB 5;  Length 4315;
     Best Local Similarity   30.5%;  Pred. No. 0.07;
RESULT 369
ID   AEA04533 standard; protein; 5178 AA.
DE   Human protein from gene under-expressed in cancer, MUC2.
PN   WO2005044990-A2.
PD   19-MAY-2005.
PA   (FARB ) BAYER HEALTHCARE LLC.
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
     Query Match     6.8%;  Score 149.5; DB 9;  Length 5178;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 370
ID   AAM24516 standard; protein; 5179 AA.
DE   C899P predicted amino acid sequence.
PN   WO200149716-A2.
PD   12-JUL-2001.

PA   (CORI-) CORIXA CORP.
     Query Match     6.8%;  Score 149.5; DB 4;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 371
ID   ABP55365 standard; protein; 5179 AA.
DE   Human colon tumour protein for clone C899P SEQ ID NO:1068.
PN   WO200283070-A2.
PD   24-OCT-2002.
PA   (CORI-) CORIXA CORP.
     Query Match     6.8%;  Score 149.5; DB 6;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 372
ID   ABO07258 standard; protein; 5179 AA.
DE   Human p53 modifying protein, SEQ ID 218.
PN   WO200299122-A1.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match     6.8%;  Score 149.5; DB 6;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 373
ID   ADD48091 standard; protein; 5179 AA.
DE   Human Protein NP_002448, SEQ ID NO 13789.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match     6.8%;  Score 149.5; DB 7;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 374
ID   ADD44998 standard; protein; 5179 AA.
DE   Human Protein Q02817, SEQ ID NO 10430.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match     6.8%;  Score 149.5; DB 7;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 375
ID   ADQ29695 standard; protein; 5179 AA.
DE   Human colorectal cancer-associated protein #50.
PN   EP1439393-A2.
PD   21-JUL-2004.
PA   (FARB ) BAYER HEALTHCARE LLC.
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
     Query Match     6.8%;  Score 149.5; DB 8;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 376
ID   ADQ80379 standard; protein; 5179 AA.
DE   Intestinal/tracheal mucin 2 protein.
PN   WO2004063709-A2.
PD   29-JUL-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
     Query Match     6.8%;  Score 149.5; DB 8;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 377
ID   AEA27639 standard; protein; 5179 AA.
DE   Human intestinal mucin.
PN   WO2005047321-A2.
PD   26-MAY-2005.
PA   (UYCR-) UNIV CREIGHTON.
     Query Match     6.8%;  Score 149.5; DB 9;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 378
ID   AEF70007 standard; protein; 5179 AA.
DE   Colorectal cancer-associated marker protein SEQ ID NO:185.
PN   WO2006015047-A2.
PD   09-FEB-2006.
PA   (FARB ) BAYER HEALTHCARE LLC.
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
     Query Match     6.8%;  Score 149.5; DB 10;  Length 5179;
     Best Local Similarity   34.1%;  Pred. No. 0.091;
RESULT 379
ID   AEI44945 standard; protein; 5179 AA.
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DE   Human mucin2 protein.
PN   WO2006061414-A1.
PD   15-JUN-2006.
PA   (INGE-) INGENIUM PHARM AG.
     Query Match   6.8%; Score 149.5; DB 10; Length 5179;
     Best Local Similarity 34.1%; Pred. No. 0.091;

RESULT 380
ID   ADL23265 standard; protein; 5703 AA.
DE   Human MUC5B.
PN   WO2004019041-A1.
PD   04-MAR-2004.
PA   (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.
PA   (PACK/) PACKER N H.
PA   (KARL/) KARLSSON N.
PA   (SCHU/) SCHULZ B L.
     Query Match   6.8%; Score 149.5; DB 8; Length 5703;
     Best Local Similarity 30.5%; Pred. No. 0.1;

RESULT 381
ID   AEI44946 standard; protein; 1233 AA.
DE   Human mucin5ac protein (C-terminal and central sequence).
PN   WO2006061414-A1.
PD   15-JUN-2006.
PA   (INGE-) INGENIUM PHARM AG.
     Query Match   6.7%; Score 148.5; DB 10; Length 1233;
     Best Local Similarity 30.1%; Pred. No. 0.014;

RESULT 382
ID   ADN18882 standard; protein; 1609 AA.
DE   Bacterial polypeptide #1535.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.7%; Score 147.5; DB 8; Length 1609;
     Best Local Similarity 22.4%; Pred. No. 0.025;

RESULT 383
ID   AAR88466 standard; protein; 629 AA.
DE   Drosophila scavenger receptor class CI.
PN   WO9600288-A2.
PD   04-JAN-1996.
PA   (MASI) MASSACHUSETTS INST TECHNOLOGY.
     Query Match   6.6%; Score 145.5; DB 2; Length 629;
     Best Local Similarity 22.9%; Pred. No. 0.0098;

RESULT 384
ID   ABG33057 standard; protein; 629 AA.
DE   Fruit fly scavenger receptor type CI (dSR-CI).
PN   US6542289-B1.
PD   06-AUG-2002.
PA   (MASI) MASSACHUSETTS INST TECHNOLOGY.
     Query Match   6.6%; Score 145.5; DB 5; Length 629;
     Best Local Similarity 22.9%; Pred. No. 0.0098;

RESULT 385
ID   AAE21524 standard; protein; 629 AA.
DE   Drosophila melanogaster scavenger receptor class CI (dSR-CI).
PN   US6350859-B1.
PD   26-FEB-2002.
PA   (MASI) MASSACHUSETTS INST TECHNOLOGY.
     Query Match   6.6%; Score 145.5; DB 5; Length 629;
     Best Local Similarity 22.9%; Pred. No. 0.0098;

RESULT 386
ID   ADT07505 standard; protein; 2109 AA.
DE   Human colon-specific polypeptide (CSP) #22.
PN   WO2004089301-A2.
PD   21-OCT-2004.
PA   (DIAD-) DIADEXUS INC.
     Query Match   6.6%; Score 145; DB 8; Length 2109;
     Best Local Similarity 28.7%; Pred. No. 0.06;

RESULT 387
ID   ADT07506 standard; protein; 2254 AA.
DE   Human colon-specific polypeptide (CSP) #23.
PN   WO2004089301-A2.
PD   21-OCT-2004.
PA   (DIAD-) DIADEXUS INC.
     Query Match   6.6%; Score 145; DB 8; Length 2254;
     Best Local Similarity 28.7%; Pred. No. 0.066;

RESULT 388
ID   ADT07507 standard; protein; 2401 AA.
DE   Human colon-specific polypeptide (CSP) #24.
PN   WO2004089301-A2.
PD   21-OCT-2004.
PA   (DIAD-) DIADEXUS INC.
     Query Match   6.6%; Score 145; DB 8; Length 2401;
     Best Local Similarity 28.7%; Pred. No. 0.072;

RESULT 389
ID   ABU53155 standard; protein; 692 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #15.
PN   WO20011659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   6.5%; Score 144.5; DB 4; Length 692;
     Best Local Similarity 29.1%; Pred. No. 0.014;

RESULT 390
ID   ABB71302 standard; protein; 787 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40698.
PN   WO20017042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.5%; Score 144.5; DB 4; Length 787;
     Best Local Similarity 21.5%; Pred. No. 0.016;

RESULT 391
ID   ADI21666 standard; protein; 1370 AA.
DE   Novel human polypeptide #145.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.5%; Score 144.5; DB 7; Length 1370;
     Best Local Similarity 22.3%; Pred. No. 0.036;

RESULT 392
ID   ADY34540 standard; protein; 1393 AA.
DE   DPCR1 (1393 amino acid form), pancreas cancer marker.
PN   WO2005019257-A1.
PD   03-MAR-2005.
PA   (CLLT) CELLTECH R & D LTD.
     Query Match   6.5%; Score 144.5; DB 9; Length 1393;
     Best Local Similarity 22.3%; Pred. No. 0.036;

RESULT 393
ID   ADN39110 standard; protein; 1460 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:428.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   6.5%; Score 144.5; DB 7; Length 1460;
     Best Local Similarity 22.3%; Pred. No. 0.039;

RESULT 394
ID   ADI21202 standard; protein; 1538 AA.
DE   Novel human protein #177.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.5%; Score 144.5; DB 7; Length 1538;
     Best Local Similarity 22.3%; Pred. No. 0.042;

RESULT 395
ID   ABU54861 standard; protein; 10431 AA.
DE   Human CA125 amino terminal extension.
PN   WO2002083866-A2.
PD   24-OCT-2002.
PA   (UYAR-) UNIV ARKANSAS.
     Query Match   6.5%; Score 144; DB 6; Length 10431;
     Best Local Similarity 24.4%; Pred. No. 0.7;

RESULT 396
ID   ADR72871 standard; protein; 22152 AA.
DE   Human ovarian cancer-related tumour marker CA125 protein.
PN   WO2004075713-A2.
PD   10-SEP-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match   6.5%; Score 144; DB 8; Length 22152;
 Best Local Similarity 24.4%; Pred. No. 2;
RESULT 397
ID ABP64957 standard; protein; 377 AA.
DE Human protein SEQ ID 617.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
 Query Match   6.5%; Score 143.5; DB 5; Length 377;
 Best Local Similarity 33.9%; Pred. No. 0.0069;
RESULT 398
ID AAO18862 standard; protein; 626 AA.
DE Murine gp100 protein.
PN EP1222928-A2.
PD 17-JUL-2002.
PA (UYZU-) UNIV ZUERICH INST MEDIZINISCHE VIROLOGIE.
 Query Match   6.5%; Score 143; DB 5; Length 626;
 Best Local Similarity 23.3%; Pred. No. 0.016;
RESULT 399
ID ADW87779 standard; protein; 648 AA.
DE Mutant bovine silver delta82-84 protein.
PN FR2857979-A1.
PD 28-JAN-2005.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (UYLI-) UNIV LIMOGES.
 Query Match   6.5%; Score 143; DB 9; Length 648;
 Best Local Similarity 24.6%; Pred. No. 0.016;
RESULT 400
ID ADW87775 standard; protein; 649 AA.
DE Bovine Silver protein.
PN FR2857979-A1.
PD 28-JAN-2005.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (UYLI-) UNIV LIMOGES.
 Query Match   6.5%; Score 143; DB 9; Length 649;
 Best Local Similarity 24.6%; Pred. No. 0.016;
RESULT 401
ID ADW87777 standard; protein; 649 AA.
DE Mutant bovine Silver G93A protein.
PN FR2857979-A1.
PD 28-JAN-2005.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (UYLI-) UNIV LIMOGES.
 Query Match   6.5%; Score 143; DB 9; Length 649;
 Best Local Similarity 24.6%; Pred. No. 0.016;
RESULT 402
ID ABB34897 standard; peptide; 1325 AA.
DE Peptide #2403 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 403
ID ABB29725 standard; peptide; 1325 AA.
DE Peptide #2376 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 404
ID ABB20314 standard; protein; 1325 AA.
DE Protein #2313 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 405
ID AAM68085 standard; protein; 1325 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28391.

PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 406
ID AAM57707 standard; protein; 1325 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27812.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 407
ID ABG49735 standard; peptide; 1325 AA.
DE Human liver peptide, SEQ ID No 28383.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 408
ID AAM03645 standard; protein; 1325 AA.
DE Peptide #2327 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 4; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 409
ID ABG37612 standard; peptide; 1325 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27277.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match   6.5%; Score 143; DB 5; Length 1325;
 Best Local Similarity 22.3%; Pred. No. 0.045;
RESULT 410
ID AEI44947 standard; protein; 4295 AA.
DE Human mucin5b protein (predicted sequence).
PN WO200061414-A1.
PD 15-JUN-2006.
PA (INGE-) INGENIUM PHARM AG.
 Query Match   6.5%; Score 143; DB 10; Length 4295;
 Best Local Similarity 28.7%; Pred. No. 0.24;
RESULT 411
ID AAE03643 standard; protein; 377 AA.
DE Human extracellular matrix and cell adhesion molecule-7 (XMAD-7).
PN WO200142285-A2.
PD 14-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
 Query Match   6.4%; Score 142.5; DB 4; Length 377;
 Best Local Similarity 31.5%; Pred. No. 0.0083;
RESULT 412
ID ADI28038 standard; protein; 377 AA.
DE ECMCAD protein 1825473CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
 Query Match   6.4%; Score 142.5; DB 5; Length 377;
 Best Local Similarity 31.5%; Pred. No. 0.0083;
RESULT 413
ID ABB71072 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40008.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
 Query Match   6.4%; Score 142; DB 4; Length 875;
 Best Local Similarity 21.4%; Pred. No. 0.03;
RESULT 414
ID ADY34542 standard; protein; 715 AA.
DE DPCR1 (715 amino acid form), pancreas cancer marker.
PN WO200501957-A1.

PD   03-MAR-2005.
PA   (CLLT) CELLTECH R & D LTD.
     Query Match   6.4%; Score 141.5; DB 9; Length 715;
     Best Local Similarity   22.6%; Pred. No. 0.025;
RESULT 415
ID   AEL00857 standard; protein; 2038 AA.
DE   Mucin-like protein associated polypeptide SEQ ID NO 173.
PN   WO200608285l-A1.
PD   10-AUG-2006.
PA   (UYTY) UNIV TOKYO.
     Query Match   6.4%; Score 141.5; DB 10; Length 2038;
     Best Local Similarity   26.2%; Pred. No. 0.11;
RESULT 416
ID   ABL00823 standard; protein; 2038 AA.
DE   Mucin-like protein associated polypeptide SEQ ID NO 139.
PN   WO200608285l-A1.
PD   10-AUG-2006.
PA   (UYTY) UNIV TOKYO.
     Query Match   6.4%; Score 141.5; DB 10; Length 2038;
     Best Local Similarity   26.2%; Pred. No. 0.11;
RESULT 417
ID   ABB59507 standard; protein; 629 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 5313.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.4%; Score 140.5; DB 4; Length 629;
     Best Local Similarity   23.7%; Pred. No. 0.025;
RESULT 418
ID   AAW06725 standard; protein; 849 AA.
DE   FLQ1 protein, involved in flocculation, derived from S.cerevisiae.
PN   JP08205900-A.
PD   13-AUG-1996.
PA   (KIRI) KIRIN BREWERY KK.
     Query Match   6.4%; Score 140.5; DB 2; Length 849;
     Best Local Similarity   21.8%; Pred. No. 0.039;
RESULT 419
ID   AAY31978 standard; protein; 625 AA.
DE   Mouse melanoma antigen gp100.
PN   WO9947102-A2.
PD   23-SEP-1999.
PA   (GENZ) GENZYME CORP.
     Query Match   6.3%; Score 139; DB 2; Length 625;
     Best Local Similarity   22.2%; Pred. No. 0.033;
RESULT 420
ID   ABB69011 standard; protein; 1371 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 33825.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.3%; Score 138.5; DB 4; Length 1371;
     Best Local Similarity   28.1%; Pred. No. 0.11;
RESULT 421
ID   AAM79998 standard; protein; 904 AA.
DE   Human protein SEQ ID NO 3644.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.2%; Score 138; DB 4; Length 904;
     Best Local Similarity   22.7%; Pred. No. 0.068;
RESULT 422
ID   ABB78250 standard; protein; 652 AA.
DE   Amino acid sequence of a human heart of glass polypeptide.
PN   WO200262205-A2.
PD   15-AUG-2002.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   6.2%; Score 137.5; DB 5; Length 652;
     Best Local Similarity   24.2%; Pred. No. 0.047;
RESULT 423
ID   ABB78248 standard; protein; 841 AA.
DE   Amino acid sequence of a zebrafish heart of glass polypeptide.
PN   WO200262205-A2.
PD   15-AUG-2002.

PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   6.2%; Score 137.5; DB 5; Length 841;
     Best Local Similarity   24.2%; Pred. No. 0.067;
RESULT 424
ID   ABB78249 standard; protein; 977 AA.
DE   Amino acid sequence of a zebrafish heart of glass polypeptide.
PN   WO200262205-A2.
PD   15-AUG-2002.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   6.2%; Score 137.5; DB 5; Length 977;
     Best Local Similarity   24.2%; Pred. No. 0.083;
RESULT 425
ID   ABB61364 standard; protein; 1049 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 10884.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.2%; Score 137.5; DB 4; Length 1049;
     Best Local Similarity   26.0%; Pred. No. 0.092;
RESULT 426
ID   ADE62075 standard; protein; 1805 AA.
DE   Rat Protein AAA85523, SEQ ID NO 8004.
PN   WO200301647S-A2.
PD   27-FEB-2003.
PA   (FARB) BAYER AG.
     Query Match   6.2%; Score 137.5; DB 7; Length 1805;
     Best Local Similarity   22.0%; Pred. No. 0.2;
RESULT 427
ID   ABB71231 standard; protein; 579 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40485.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.2%; Score 137; DB 4; Length 579;
     Best Local Similarity   26.5%; Pred. No. 0.043;
RESULT 428
ID   ADN19290 standard; protein; 503 AA.
DE   Bacterial polypeptide #1943.
PN   US200323367S-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.2%; Score 136; DB 8; Length 503;
     Best Local Similarity   27.2%; Pred. No. 0.043;
RESULT 429
ID   AEG51912 standard; protein; 503 AA.
DE   Stress-related protein, SRP, SEQ ID NO 170.
PN   WO200603270S-A2.
PD   30-MAR-2006.
PA   (BADI) BASF PLANT SCI GMBH.
     Query Match   6.2%; Score 136; DB 10; Length 503;
     Best Local Similarity   27.2%; Pred. No. 0.043;
RESULT 430
ID   ABJ18914 standard; protein; 2261 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID No 60.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
     Query Match   6.2%; Score 136; DB 6; Length 2261;
     Best Local Similarity   21.3%; Pred. No. 0.36;
RESULT 431
ID   AEL96913 standard; protein; 2261 AA.
DE   Staphylococcus aureus ORF0398 full-length protein.
PN   WO200612166-A2.
PD   16-NOV-2006.
PA   (MERI) MERCK & CO INC.
     Query Match   6.2%; Score 136; DB 10; Length 2261;
     Best Local Similarity   21.3%; Pred. No. 0.36;
RESULT 432

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ID   AAY95559 standard; protein; 2870 AA.
DE   Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN   WO200040711-A2.
PD   13-JUL-2000.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
     Query Match             6.2%;  Score 136;  DB 3;  Length 2870;
     Best Local Similarity   23.6%;  Pred. No. 0.51;
RESULT 433
ID   ADN07634 standard; protein; 2870 AA.
DE   Caenorhabditis elegans LOV -1 deletion mutant protein.
PN   US6723557-B1.
PD   20-APR-2004.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
     Query Match             6.2%;  Score 136;  DB 8;  Length 2870;
     Best Local Similarity   23.6%;  Pred. No. 0.51;
RESULT 434
ID   ADW79951 standard; protein; 2870 AA.
DE   Nematode location of vulva (lov-1) mutant protein.
PN   US6849717-B1.
PD   01-FEB-2005.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
     Query Match             6.2%;  Score 136;  DB 9;  Length 2870;
     Best Local Similarity   23.6%;  Pred. No. 0.51;
RESULT 435
ID   AAY95556 standard; protein; 3178 AA.
DE   Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN   WO200040711-A2.
PD   13-JUL-2000.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
     Query Match             6.2%;  Score 136;  DB 3;  Length 3178;
     Best Local Similarity   23.6%;  Pred. No. 0.59;
RESULT 436
ID   ADN07623 standard; protein; 3178 AA.
DE   Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN   US6723557-B1.
PD   20-APR-2004.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
     Query Match             6.2%;  Score 136;  DB 8;  Length 3178;
     Best Local Similarity   23.6%;  Pred. No. 0.59;
RESULT 437
ID   ADW79940 standard; protein; 3178 AA.
DE   Nematode location of vulva (lov-1) protein.
PN   US6849717-B1.
PD   01-FEB-2005.
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
     Query Match             6.2%;  Score 136;  DB 9;  Length 3178;
     Best Local Similarity   23.6%;  Pred. No. 0.59;
RESULT 438
ID   ADY19014 standard; protein; 2000 AA.
DE   PRO polypeptide SEQ ID NO 4820.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match             6.1%;  Score 135.5;  DB 9;  Length 2000;
     Best Local Similarity   27.1%;  Pred. No. 0.34;
RESULT 439
ID   ABU16000 standard; protein; 2271 AA.
DE   Protein encoded by Prokaryotic essential gene #1527.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.1%;  Score 135.5;  DB 6;  Length 2271;
     Best Local Similarity   21.1%;  Pred. No. 0.4;
RESULT 440
ID   ABR92087 standard; protein; 2701 AA.
DE   Human cervical cancer cell marker encoding cDNA SEQ ID NO:83.
PN   WO2002101075-A2.
PD   19-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             6.1%;  Score 135.5;  DB 6;  Length 2701;
     Best Local Similarity   27.1%;  Pred. No. 0.51;
RESULT 441
ID   ADX05907 standard; protein; 2701 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 472.
PN   WO2005012875-A2.
PD   10-FEB-2005.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
     Query Match             6.1%;  Score 135.5;  DB 9;  Length 2701;
     Best Local Similarity   27.1%;  Pred. No. 0.51;
RESULT 442
ID   AEL84673 standard; protein; 2701 AA.
DE   Tumor marker gene BAT2D1 SEQ ID NO 40.
PN   WO200611 0593-A2.
PD   19-OCT-2006.
PA   (MACR-) MACROGENICS INC.
     Query Match             6.1%;  Score 135.5;  DB 10;  Length 2701;
     Best Local Similarity   27.1%;  Pred. No. 0.51;
RESULT 443
ID   AAB35408 standard; protein; 2819 AA.
DE   Human 07CG27 gene protein.
PN   WO200116291-A2.
PD   08-MAR-2001.
PA   (MYRI-) MYRIAD GENETICS INC.
PA   (HOSP-) HOSPITAL FOR SICK CHILDREN.
     Query Match             6.1%;  Score 135.5;  DB 4;  Length 2819;
     Best Local Similarity   27.1%;  Pred. No. 0.55;
RESULT 444
ID   ADQ97653 standard; protein; 2819 AA.
DE   Human cancer associated sequence HP10-021, SEQ ID 630.
PN   WO2004060304-A2.
PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match             6.1%;  Score 135.5;  DB 8;  Length 2819;
     Best Local Similarity   27.1%;  Pred. No. 0.55;
RESULT 445
ID   ADY34546 standard; protein; 759 AA.
DE   DPCR1 (759 amino acid form), pancreas cancer marker.
PN   WO2005019257-A1.
PD   03-MAR-2005.
PA   (CLLT ) CELLTECH R & D LTD.
     Query Match             6.1%;  Score 135;  DB 9;  Length 759;
     Best Local Similarity   22.0%;  Pred. No. 0.093;
RESULT 446
ID   AAM79014 standard; protein; 803 AA.
DE   Human protein SEQ ID NO 1676.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSB-) HYSEQ INC.
     Query Match             6.1%;  Score 135;  DB 4;  Length 803;
     Best Local Similarity   23.1%;  Pred. No. 0.1;
RESULT 447
ID   ADJ69549 standard; protein; 803 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1355.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match             6.1%;  Score 135;  DB 7;  Length 803;
     Best Local Similarity   23.1%;  Pred. No. 0.1;
RESULT 448
ID   ABO58551 standard; protein; 803 AA.
DE   Human genome derived single exon protein #4785.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
     Query Match             6.1%;  Score 135;  DB 8;  Length 803;
     Best Local Similarity   23.1%;  Pred. No. 0.1;
RESULT 449
ID   ABB69806 standard; protein; 1795 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             6.1%;  Score 134.5;  DB 4;  Length 1795;
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Best Local Similarity    25.9%;   Pred. No. 0.35;
RESULT 450
ID   ABU53165 standard; protein; 143 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #25.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match             6.1%;   Score 134;  DB 4;  Length 143;
Best Local Similarity   32.5%;   Pred. No. 0.011;
RESULT 451
ID   ABB70548 standard; protein; 838 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 38436.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Query Match             6.0%;   Score 133.5;  DB 4;  Length 838;
Best Local Similarity   24.4%;   Pred. No. 0.14;
RESULT 452
ID   ADN23131 standard; protein; 3507 AA.
DE   Bacterial polypeptide #5784.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match             6.0%;   Score 133.5;  DB 8;  Length 3507;
Best Local Similarity   22.4%;   Pred. No. 1.1;
RESULT 453
ID   ADK13881 standard; protein; 417 AA.
DE   Murine Selp1 (selectin, platelet [p-selectin ligand) protein.
PN   WO2004012817-A2.
PD   12-FEB-2004.
PA   (KYLI-) KYLIX BV.
Query Match             6.0%;   Score 133;  DB 8;  Length 417;
Best Local Similarity   24.0%;   Pred. No. 0.058;
RESULT 454
ID   ADN19365 standard; protein; 556 AA.
DE   Bacterial polypeptide #2018.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match             6.0%;   Score 133;  DB 8;  Length 556;
Best Local Similarity   22.8%;   Pred. No. 0.088;
RESULT 455
ID   ADS43638 standard; protein; 1075 AA.
DE   Bacterial polypeptide #22068.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match             6.0%;   Score 133;  DB 8;  Length 1075;
Best Local Similarity   22.6%;   Pred. No. 0.22;
RESULT 456
ID   ABB71133 standard; protein; 1277 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40191.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Query Match             6.0%;   Score 133;  DB 4;  Length 1277;
Best Local Similarity   20.2%;   Pred. No. 0.28;
RESULT 457
ID   ABG23390 standard; protein; 1209 AA.
DE   Novel human diagnostic protein #23381.
PN   WO200175067-A2.

PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match             6.0%;   Score 132.5;  DB 4;  Length 1209;
Best Local Similarity   21.9%;   Pred. No. 0.29;
RESULT 458
ID   ABM72734 standard; protein; 2271 AA.
DE   Staphylococcus aureus protein #1974.
PN   WO20294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
Query Match             6.0%;   Score 132.5;  DB 6;  Length 2271;
Best Local Similarity   21.6%;   Pred. No. 0.71;
RESULT 459
ID   ABP56876 standard; protein; 2283 AA.
DE   Staphylococcus epidermidis DsqA protein SEQ ID NO:4.
PN   WO200210829-A2.
PD   27-DEC-2002.
PA   (INHI-) INHIBITEX INC.
PA   (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA   (UYPA-) UNIV PAVIA.
Query Match             6.0%;   Score 132.5;  DB 6;  Length 2283;
Best Local Similarity   21.6%;   Pred. No. 0.71;
RESULT 460
ID   AAY54466 standard; protein; 788 AA.
DE   Amino acid sequence of intestinal insect mucin isoform IIM14.
PN   WO996373-A2.
PD   29-DEC-1999.
PA   (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match             6.0%;   Score 132;  DB 3;  Length 788;
Best Local Similarity   31.0%;   Pred. No. 0.17;
RESULT 461
ID   AAY54467 standard; protein; 807 AA.
DE   Amini acid sequence of intestinal insect mucin isoform IIM22.
PN   WO996373-A2.
PD   29-DEC-1999.
PA   (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match             6.0%;   Score 132;  DB 3;  Length 807;
Best Local Similarity   31.0%;   Pred. No. 0.18;
RESULT 462
ID   ADC21533 standard; protein; 1162 AA.
DE   T.cruzi trans-sialidase, TS, clone 7F.
PN   US2002137667-A1.
PD   26-SEP-2002.
PA   (TUFT ) UNIV TUFTS.
Query Match             6.0%;   Score 132;  DB 7;  Length 1162;
Best Local Similarity   22.2%;   Pred. No. 0.3;
RESULT 463
ID   AEL43168 standard; protein; 1162 AA.
DE   T.cruzi neuraminidase (TCNA) protein.
PN   US200629247-A1.
PD   12-OCT-2006.
PA   (CHUE/) CHUENKOVA M.
PA   (PERE/) PEREIRA M A.
Query Match             6.0%;   Score 132;  DB 10;  Length 1162;
Best Local Similarity   22.2%;   Pred. No. 0.3;
RESULT 464
ID   ADM68815 standard; protein; 5317 AA.
DE   Sea urchin ryanodine receptor related protein SEQ ID NO:59.
PN   WO2004027042-A2.
PD   01-APR-2004.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match             5.9%;   Score 131.5;  DB 8;  Length 5317;
Best Local Similarity   24.9%;   Pred. No. 2.9;
RESULT 465
ID   ABO59505 standard; protein; 301 AA.
DE   Human genome derived single exon protein #5739.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
Query Match             5.9%;   Score 131;  DB 8;  Length 301;
Best Local Similarity   28.6%;
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RESULT 466
ID   ABB70781 standard; protein; 337 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 39135.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.9%; Score 131; DB 4; Length 337;
     Best Local Similarity   28.2%; Pred. No. 0.063;
RESULT 467
ID   ADN19351 standard; protein; 725 AA.
DE   Bacterial polypeptide #2004.
PN   US20033233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   5.9%; Score 131; DB 8; Length 725;
     Best Local Similarity   19.5%; Pred. No. 0.19;
RESULT 468
ID   ABB70377 standard; protein; 1428 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.9%; Score 131; DB 4; Length 1428;
     Best Local Similarity   25.3%; Pred. No. 0.49;
RESULT 469
ID   ADY09213 standard; protein; 646 AA.
DE   Plant full length insert polypeptide seqid 65028.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   5.9%; Score 130.5; DB 8; Length 646;
     Best Local Similarity   23.6%; Pred. No. 0.17;
RESULT 470
ID   ABP43882 standard; protein; 459 AA.
DE   Human EXMAD-20 protein.
PN   WO200231111-A2.
PD   18-APR-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.9%; Score 130; DB 5; Length 459;
     Best Local Similarity   20.9%; Pred. No. 0.12;
RESULT 471
ID   ADD48958 standard; protein; 548 AA.
DE   Rat Protein U89744, SEQ ID NO 14670.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.9%; Score 130; DB 7; Length 548;
     Best Local Similarity   30.2%; Pred. No. 0.15;
RESULT 472
ID   AAP91941 standard; peptide; 400 AA.
DE   Sequence of preprospasmolysin.
PN   DE3808456-A.
PD   28-SEP-1989.
PA   (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
     Query Match   5.9%; Score 129.5; DB 1; Length 400;
     Best Local Similarity   20.9%; Pred. No. 0.11;
RESULT 473
ID   AAB11743 standard; protein; 175 AA.
DE   C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:17.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.8%; Score 129; DB 3; Length 175;

     Best Local Similarity   27.3%; Pred. No. 0.036;
RESULT 474
ID   ABJ04056 standard; protein; 175 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 17.
PN   WO200194631-A1.
PD   13-DEC-2001.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.8%; Score 129; DB 5; Length 175;
     Best Local Similarity   27.3%; Pred. No. 0.036;
RESULT 475
ID   ABP70440 standard; protein; 365 AA.
DE   Amino acid sequence of human TIM-1 allele 3.
PN   WO2003002722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.8%; Score 129; DB 6; Length 365;
     Best Local Similarity   23.4%; Pred. No. 0.1;
RESULT 476
ID   ADY98075 standard; protein; 365 AA.
DE   Human TIM-1 allele 3-encoded protein.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
PA   (DAND) DANA FARBER CANCER INST INC.
     Query Match   5.8%; Score 129; DB 9; Length 365;
     Best Local Similarity   23.4%; Pred. No. 0.1;
RESULT 477
ID   AED60519 standard; protein; 365 AA.
DE   Human TIM-1, allele 3, protein SEQ ID NO:27.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
     Query Match   5.8%; Score 129; DB 9; Length 365;
     Best Local Similarity   23.4%; Pred. No. 0.1;
RESULT 478
ID   ABU53164 standard; protein; 492 AA.
DE   Human testes-derived DKF2phtes3_2a11 homologue #24.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.8%; Score 129; DB 4; Length 492;
     Best Local Similarity   29.4%; Pred. No. 0.16;
RESULT 479
ID   ABU53152 standard; protein; 695 AA.
DE   Human testes-derived DKF2phtes3_2a11 homologue #12.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.8%; Score 129; DB 4; Length 695;
     Best Local Similarity   29.4%; Pred. No. 0.26;
RESULT 480
ID   ABU53142 standard; protein; 745 AA.
DE   Human testes-derived DKF2phtes3_2a11 homologue #2.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.8%; Score 129; DB 4; Length 745;
     Best Local Similarity   29.4%; Pred. No. 0.28;
RESULT 481
ID   ABU53154 standard; protein; 745 AA.
DE   Human testes-derived DKF2phtes3_2a11 homologue #14.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.8%; Score 129; DB 4; Length 745;
     Best Local Similarity   29.4%; Pred. No. 0.28;
RESULT 482
ID   ABU53141 standard; protein; 770 AA.
DE   Human testes-derived DKF2phtes3_2a11 homologue #1.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.8%; Score 129; DB 4; Length 770;

Best Local Similarity   29.4%;   Pred. No. 0.3;
RESULT 483
ID   ABUS3143 standard; protein; 778 AA.
DE   Human testes-derived DKFZphtes3_2a11 homologue #3.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.8%;   Score 129;   DB 4;   Length 778;
     Best Local Similarity   29.4%;   Pred. No. 0.3;
RESULT 484
ID   ABG70111 standard; protein; 1488 AA.
DE   Human prey protein for Shigella ospC1 #29.
PN   WO200257303-A2.
PD   25-JUL-2002.
PA   (HYBR-) HYBRIGENICS.
     Query Match   5.8%;   Score 129;   DB 5;   Length 1488;
     Best Local Similarity   22.9%;   Pred. No. 0.75;
RESULT 485
ID   ADJ68961 standard; protein; 2011 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID767.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   5.8%;   Score 129;   DB 7;   Length 2011;
     Best Local Similarity   22.9%;   Pred. No. 1.2;
RESULT 486
ID   ADO44003 standard; protein; 2011 AA.
DE   Amino acid sequence of upstream regulatory element binding protein 1.
PN   WO2004031242-A2.
PD   15-APR-2004.
PA   (CELL-) CELLZOME AG.
     Query Match   5.8%;   Score 129;   DB 7;   Length 2011;
     Best Local Similarity   22.9%;   Pred. No. 1.2;
RESULT 487
ID   ADS11077 standard; protein; 2309 AA.
DE   Human therapeutic protein - SEQ ID 1314.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
     Query Match   5.8%;   Score 129;   DB 8;   Length 2309;
     Best Local Similarity   22.9%;   Pred. No. 1.4;
RESULT 488
ID   ADE78997 standard; protein; 4374 AA.
DE   Human protein modification and maintenance molecule (PMMM)-35.
PN   WO2003063688-A2.
PD   07-AUG-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   5.8%;   Score 129;   DB 7;   Length 4374;
     Best Local Similarity   22.9%;   Pred. No. 3.5;
RESULT 489
ID   AEF92980 standard; protein; 4374 AA.
DE   Human HectH9 protein sequence.
PN   WO2006018654-A1.
PD   23-FEB-2006.
PA   (CANC-) CANCER RES TECHNOLOGY LTD.
     Query Match   5.8%;   Score 129;   DB 10;   Length 4374;
     Best Local Similarity   22.9%;   Pred. No. 3.5;
RESULT 490
ID   AEG65350 standard; protein; 4374 AA.
DE   Human ARF-BP1 polypeptide.
PN   WO2006031928-A2.
PD   23-MAR-2006.
PA   (UYCO) UNIV COLUMBIA NEW YORK.
     Query Match   5.8%;   Score 129;   DB 10;   Length 4374;
     Best Local Similarity   22.9%;   Pred. No. 3.5;
RESULT 491
ID   AEG97364 standard; protein; 634 AA.
DE   C. albicans cell wall protein HWP1 SEQ ID NO 133.
PN   WO2006036817-A2.
PD   06-APR-2006.
PA   (MICR-) MICROBIA INC.
     Query Match   5.8%;   Score 128.5;   DB 10;   Length 634;

Best Local Similarity   22.1%;   Pred. No. 0.25;
RESULT 492
ID   AAB11746 standard; protein; 249 AA.
DE   C. parvum NINC isolate GP900 variant domain 2, SEQ ID NO:20.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.8%;   Score 128;   DB 3;   Length 249;
     Best Local Similarity   26.0%;   Pred. No. 0.072;
RESULT 493
ID   ABJ04059 standard; protein; 249 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 20.
PN   WO20019463l-A1.
PD   13-DEC-2001.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.8%;   Score 128;   DB 5;   Length 249;
     Best Local Similarity   26.0%;   Pred. No. 0.072;
RESULT 494
ID   ADS43586 standard; protein; 605 AA.
DE   Bacterial polypeptide #22016.
PN   US20033675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   5.8%;   Score 128;   DB 8;   Length 605;
     Best Local Similarity   23.2%;   Pred. No. 0.25;
RESULT 495
ID   ABR53287 standard; protein; 870 AA.
DE   Protein sequence #SEQ ID 1439.
PN   EP1258494-A1.
PD   20-NOV-2002.
PA   (CELL-) CELLZOME AG.
     Query Match   5.8%;   Score 128;   DB 6;   Length 870;
     Best Local Similarity   22.2%;   Pred. No. 0.43;
RESULT 496
ID   ADK63574 standard; protein; 870 AA.
DE   Disease treating protein complex-derived protein #866.
PN   EP1138608-A2.
PD   27-AUG-2003.
PA   (CELL-) CELLZOME AG.
     Query Match   5.8%;   Score 128;   DB 7;   Length 870;
     Best Local Similarity   22.2%;   Pred. No. 0.43;
RESULT 497
ID   ADY07297 standard; protein; 1989 AA.
DE   Plant full length insert polypeptide seqid 63112.
PN   US200034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   5.8%;   Score 128;   DB 8;   Length 1989;
     Best Local Similarity   22.7%;   Pred. No. 1.4;
RESULT 498
ID   AAY37173 standard; protein; 424 AA.
DE   Amino acid sequence of a Chlamydia trachomatis protein.
PN   WO992475-A2.
PD   10-JUN-1999.
PA   (GEST) GENSET.
     Query Match   5.8%;   Score 127.5;   DB 2;   Length 424;
     Best Local Similarity   25.5%;   Pred. No. 0.17;
RESULT 499
ID   ADS51624 standard; protein; 558 AA.
DE   Human CAF-1 p60 protein.
PN   WO2004085644-A2.
PD   07-OCT-2004.
PA   (BADI) BASF PLANT SCI GMBH.
     Query Match   5.8%;   Score 127.5;   DB 8;   Length 558;

Best Local Similarity 21.9%; Pred. No. 0.25;
RESULT 500
ID ADM05244 standard; protein; 577 AA.
DE Human protein of the invention SEQ ID NO:3929.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 127.5; DB 7; Length 577;
Best Local Similarity 21.9%; Pred. No. 0.26;
RESULT 501
ID AEC88174 standard; protein; 577 AA.
DE Human cDNA clone protein PROST20100460, SEQ ID 3929.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 127.5; DB 9; Length 577;
Best Local Similarity 21.9%; Pred. No. 0.26;
RESULT 502
ID AEG97295 standard; protein; 634 AA.
DE C. albicans hyphal growth regulator HWP1 SEQ ID NO 64.
PN WO2006036817-A2.
PD 06-APR-2006.
PA (MICR-) MICROBIA INC.
Query Match 5.8%; Score 127.5; DB 10; Length 634;
Best Local Similarity 21.8%; Pred. No. 0.3;
RESULT 503
ID ADQ67713 standard; protein; 933 AA.
DE Novel human protein sequence #2379.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 127.5; DB 8; Length 933;
Best Local Similarity 23.0%; Pred. No. 0.52;
RESULT 504
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.7%; Score 127; DB 2; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 505
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.7%; Score 127; DB 2; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 506
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.7%; Score 127; DB 4; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 507
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 5.7%; Score 127; DB 4; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 508
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.7%; Score 127; DB 7; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;

RESULT 509
ID ADG17394 standard; protein; 288 AA.
DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 5.7%; Score 127; DB 7; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 510
ID AEH92887 standard; protein; 288 AA.
DE T. gondii polypeptide PTG(288) SEQ ID NO: 341.
PN US2006115496-A1.
PD 01-JUN-2006.
PA (MILH/) MILHAUSEN M J.
Query Match 5.7%; Score 127; DB 10; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 511
ID AEH92890 standard; protein; 288 AA.
DE T. gondii nTG(1397) encoded polypeptide SEQ ID NO: 344.
PN US2006115496-A1.
PD 01-JUN-2006.
PA (MILH/) MILHAUSEN M J.
Query Match 5.7%; Score 127; DB 10; Length 288;
Best Local Similarity 21.2%; Pred. No. 0.11;
RESULT 512
ID AAR66810 standard; peptide; 357 AA.
DE Extracellular domain of mouse syndecan-3 protein.
PN WO9500633-A2.
PD 05-JAN-1995.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.7%; Score 127; DB 2; Length 357;
Best Local Similarity 26.3%; Pred. No. 0.15;
RESULT 513
ID AEI26926 standard; protein; 1260 AA.
DE Candida albicans agglutinin-like sequence 1, SEQ ID NO: 8.
PN US7067138-B1.
PD 27-JUN-2006.
PA (ANGE-) LOS ANGELES BIOMEDICAL RES INST AT HARBO.
Query Match 5.7%; Score 127; DB 10; Length 1260;
Best Local Similarity 21.4%; Pred. No. 0.87;
RESULT 514
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO20024340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 127; DB 5; Length 1296;
Best Local Similarity 22.1%; Pred. No. 0.91;
RESULT 515
ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO20024340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 127; DB 5; Length 1296;
Best Local Similarity 22.1%; Pred. No. 0.91;
RESULT 516
ID ADN18700 standard; protein; 1322 AA.
DE Bacterial polypeptide #1353.
PN US200233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 127; DB 8; Length 1322;
Best Local Similarity 21.0%; Pred. No. 0.93;
RESULT 517
ID ABU62115 standard; protein; 1446 AA.
DE Rat and human, RIZ1, DNA consensus sequence.
PN US200303266-A1

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PD   13-FEB-2003.
PA   (HUAN/) HUANG S.
PA   (CHAD/) CHADWICK R B.
     Query Match          5.7%;    Score 127;  DB 6;   Length 1446;
     Best Local Similarity  22.1%;   Pred. No. 1.1;
RESULT 518
ID   ADY34544 standard; protein; 552 AA.
DE   DPCR1 (552 amino acid form), pancreas cancer marker.
PN   WO2005019257-A1.
PD   03-MAR-2005.
PA   (CLLT ) CELLTECH R & D LTD.
     Query Match          5.7%;    Score 126.5;  DB 9;   Length 552;
     Best Local Similarity  21.9%;   Pred. No. 0.3;
RESULT 519
ID   ADX83203 standard; protein; 982 AA.
DE   Human TEG26 polypeptide SEQ ID NO 85.
PN   WO2005014818-A1.
PD   17-FEB-2005.
PA   (PERS ) PERSEUS PROTEOMICS INC.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PA   (ABUR/) ABURATANI H.
     Query Match          5.7%;    Score 126.5;  DB 9;   Length 982;
     Best Local Similarity  24.4%;   Pred. No. 0.67;
RESULT 520
ID   ADC31682 standard; protein; 1205 AA.
DE   Human novel polypeptide sequence, SEQ ID NO:1764.
PN   WO2003029271-A2.
PD   10-APR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match          5.7%;    Score 126.5;  DB 7;   Length 1205;
     Best Local Similarity  23.2%;   Pred. No. 0.9;
RESULT 521
ID   ABW01168 standard; protein; 1260 AA.
DE   Candida albicans agglutinin-like sequence (ALS) 1 protein.
PN   US2003124134-A1.
PD   03-JUL-2003.
PA   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
     Query Match          5.7%;    Score 126.5;  DB 7;   Length 1260;
     Best Local Similarity  21.4%;   Pred. No. 0.96;
RESULT 522
ID   AEG97341 standard; protein; 1260 AA.
DE   C. albicans cell wall protein ALS1b SEQ ID NO 110.
PN   WO2006036817-A2.
PD   06-APR-2006.
PA   (MICR-) MICROBIA INC.
     Query Match          5.7%;    Score 126.5;  DB 10;   Length 1260;
     Best Local Similarity  21.4%;   Pred. No. 0.96;
RESULT 523
ID   AAB11726 standard; protein; 1837 AA.
DE   Cryptosporidium parvum Iowa isolate GP900.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match          5.7%;    Score 126.5;  DB 3;   Length 1837;
     Best Local Similarity  21.4%;   Pred. No. 1.6;
RESULT 524
ID   ABJ04044 standard; protein; 1837 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 5.
PN   WO200194631-A1.
PD   13-DEC-2001.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match          5.7%;    Score 126.5;  DB 5;   Length 1837;
     Best Local Similarity  22.3%;   Pred. No. 1.6;
RESULT 525
ID   ADR18914 standard; protein; 2240 AA.
DE   Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
PN   WO2004069136-A2.
PD   19-AUG-2004.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
     Query Match          5.7%;    Score 126.5;  DB 8;   Length 2240;
     Best Local Similarity  25.6%;   Pred. No. 2.2;
RESULT 526
ID   ADR18913 standard; protein; 2258 AA.
DE   Human mucin-like protein, SCS0004, variant SEQ ID 3.
PN   WO2004069136-A2.
PD   19-AUG-2004.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
     Query Match          5.7%;    Score 126.5;  DB 8;   Length 2258;
     Best Local Similarity  25.6%;   Pred. No. 2.2;
RESULT 527
ID   ADR18915 standard; protein; 2264 AA.
DE   His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
PN   WO2004069136-A2.
PD   19-AUG-2004.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
     Query Match          5.7%;    Score 126.5;  DB 8;   Length 2264;
     Best Local Similarity  25.6%;   Pred. No. 2.2;
RESULT 528
ID   ADO28930 standard; protein; 2481 AA.
DE   Human novel GPCR PGR17, SEQ ID NO:29.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match          5.7%;    Score 126.5;  DB 8;   Length 2481;
     Best Local Similarity  20.7%;   Pred. No. 2.5;
RESULT 529
ID   ABG06375 standard; protein; 2570 AA.
DE   Novel human diagnostic protein #6366.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match          5.7%;    Score 126.5;  DB 4;   Length 2570;
     Best Local Similarity  20.7%;   Pred. No. 2.6;
RESULT 530
ID   ABG20119 standard; protein; 2724 AA.
DE   Novel human diagnostic protein #20110.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match          5.7%;    Score 126.5;  DB 4;   Length 2724;
     Best Local Similarity  25.1%;   Pred. No. 2.9;
RESULT 531
ID   AAB20164 standard; protein; 608 AA.
DE   Human protein associated with IgA nephropathy.
PN   WO200105803-A1.
PD   25-JAN-2001.
PA   (GENE-) GENE LOGIC INC.
     Query Match          5.7%;    Score 126;  DB 4;   Length 608;
     Best Local Similarity  21.1%;   Pred. No. 0.37;
RESULT 532
ID   ABB61005 standard; protein; 777 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 9807.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match          5.7%;    Score 126;  DB 4;   Length 777;
     Best Local Similarity  30.8%;   Pred. No. 0.53;
RESULT 533
ID   ADC31624 standard; protein; 1946 AA.
DE   Human novel polypeptide sequence, SEQ ID NO:1706.
PN   WO2003029271-A2.
PD   10-APR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match          5.7%;    Score 126;  DB 7;   Length 1946;
     Best Local Similarity  24.4%;   Pred. No. 2;
RESULT 534
ID   AAB27242 standard; protein; 571 AA.
DE   Human EXMAD-20 SEQ ID NO: 20.
PN   WO200068380-A2.
PD   16-NOV-2000.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match          5.7%;    Score 125.5;  DB 4;   Length 571;
     Best Local Similarity  27.9%;   Pred. No. 0.38;
RESULT 535
ID   ABB71280 standard; protein; 588 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40632.
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PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.7%; Score 125.5; DB 4; Length 588;
    Best Local Similarity 23.2%; Pred. No. 0.39;
RESULT 536
ID ADH71762 standard; protein; 834 AA.
DE Human protein of the invention NOV28k SEQ ID NO:658.
PN WO200102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
    Query Match   5.7%; Score 125.5; DB 8; Length 834;
    Best Local Similarity 20.0%; Pred. No. 0.64;
RESULT 537
ID ABB68509 standard; protein; 1301 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32319.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.7%; Score 125.5; DB 4; Length 1301;
    Best Local Similarity 25.5%; Pred. No. 1.2;
RESULT 538
ID ABR82116 standard; protein; 1458 AA.
DE Human ALMS2 tandem amino acid repeat region 498-1958.
PN WO200034072-A2.
PD 24-APR-2003.
PA (UYSO-) UNIV SOUTHAMPTON.
    Query Match   5.7%; Score 125.5; DB 4; Length 1458;
    Best Local Similarity 22.8%; Pred. No. 1.4;
RESULT 539
ID AED20795 standard; protein; 1602 AA.
DE ALMS1 related human protein, SEQ ID 97.
PN US2005214757-A1.
PD 29-SEP-2005.
PA (WILS/) WILSON D I.
PA (HEAR/) HEARN T.
PA (WALK/) WALKER M.
    Query Match   5.7%; Score 125.5; DB 9; Length 1602;
    Best Local Similarity 22.8%; Pred. No. 1.6;
RESULT 540
ID AAW48299 standard; protein; 1721 AA.
DE Cryptosporidium parvum GP900 antigen.
PN WO9806430-A1.
PD 19-FEB-1998.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.7%; Score 125.5; DB 2; Length 1721;
    Best Local Similarity 21.6%; Pred. No. 1.8;
RESULT 541
ID AAB11727 standard; protein; 1721 AA.
DE Portion of Cryptosporidium parvum NINC isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.7%; Score 125.5; DB 3; Length 1721;
    Best Local Similarity 21.6%; Pred. No. 1.8;
RESULT 542
ID ABJ04045 standard; protein; 1721 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 6.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.7%; Score 125.5; DB 5; Length 1721;
    Best Local Similarity 21.6%; Pred. No. 1.8;
RESULT 543
ID ABM85423 standard; protein; 3708 AA.
DE Human protein sequence hCP50502.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
    Query Match   5.7%; Score 125.5; DB 7; Length 3708;
    Best Local Similarity 22.8%; Pred. No. 5.3;
RESULT 544
ID ABR82115 standard; protein; 4127 AA.

DE Human ALMS1 protein sequence.
PN WO200034072-A2.
PD 24-APR-2003.
PA (UYSO-) UNIV SOUTHAMPTON.
    Query Match   5.7%; Score 125.5; DB 6; Length 4127;
    Best Local Similarity 22.8%; Pred. No. 6.2;
RESULT 545
ID AED20701 standard; protein; 4127 AA.
DE Human ALMS1 protein, SEQ ID 3.
PN US2005214757-A1.
PD 29-SEP-2005.
PA (WILS/) WILSON D I.
PA (HEAR/) HEARN T.
PA (WALK/) WALKER M.
    Query Match   5.7%; Score 125.5; DB 9; Length 4127;
    Best Local Similarity 22.8%; Pred. No. 6.2;
RESULT 546
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
    Query Match   5.7%; Score 125; DB 7; Length 235;
    Best Local Similarity 23.9%; Pred. No. 0.12;
RESULT 547
ID ADZ11122 standard; protein; 2033 AA.
DE Murine cancer-associated protein #70.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
    Query Match   5.7%; Score 125; DB 9; Length 2033;
    Best Local Similarity 23.9%; Pred. No. 2.5;
RESULT 548
ID ABP39618 standard; protein; 2137 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4463.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   5.7%; Score 125; DB 5; Length 2137;
    Best Local Similarity 20.5%; Pred. No. 2.7;
RESULT 549
ID ADS05656 standard; protein; 2137 AA.
DE Staphylococcus epidermis polypeptide seqid 4951.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
    Query Match   5.7%; Score 125; DB 8; Length 2137;
    Best Local Similarity 20.5%; Pred. No. 2.7;
RESULT 550
ID AEI11739 standard; protein; 2137 AA.
DE Staphylococcus epidermidis protein amino acid sequence - SEQ ID 4951.
PN US7060458-B1.
PD 13-JUN-2006.
PA (AMHP) WYETH.
    Query Match   5.7%; Score 125; DB 10; Length 2137;
    Best Local Similarity 20.5%; Pred. No. 2.7;
RESULT 551
ID ABP70442 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
    Query Match   5.6%; Score 124.5; DB 6; Length 364;
    Best Local Similarity 23.7%; Pred. No. 0.24;
RESULT 552
ID ADY98079 standard; protein; 364 AA.
DE Human TIM-1 allele 5-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.

Query Match   5.6%;   Score 124.5;   DB 9;   Length 364;
Best Local Similarity   23.7%;   Pred. No. 0.24;
RESULT 553
ID   AED60523 standard; protein; 364 AA.
DE   Human TIM-1, allele 5, protein SEQ ID NO.31.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
Query Match   5.6%;   Score 124.5;   DB 9;   Length 364;
Best Local Similarity   23.7%;   Pred. No. 0.24;
RESULT 554
ID   AAB95295 standard; protein; 500 AA.
DE   Human protein sequence SEQ ID NO:17521.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
Query Match   5.6%;   Score 124.5;   DB 4;   Length 500;
Best Local Similarity   21.1%;   Pred. No. 0.38;
RESULT 555
ID   AAG77967 standard; protein; 500 AA.
DE   Human hepatocyte growth factor activator inhibitor (HGF-AIh) #2.
PN   WO200168707-A1.
PD   20-SEP-2001.
PA   (ELIL) LILLY & CO ELI.
Query Match   5.6%;   Score 124.5;   DB 5;   Length 500;
Best Local Similarity   21.1%;   Pred. No. 0.38;
RESULT 556
ID   AAE17603 standard; protein; 500 AA.
DE   Human extracellular messenger (XMES)-5 protein.
PN   WO200194587-A2.
PD   13-DEC-2001.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match   5.6%;   Score 124.5;   DB 5;   Length 500;
Best Local Similarity   21.1%;   Pred. No. 0.38;
RESULT 557
ID   ADT87028 standard; protein; 1306 AA.
DE   Yeast stress-related protein from gene YR014W.
PN   WO2004092398-A2.
PD   28-OCT-2004.
PA   (BADI) BASF PLANT SCI GMBH.
Query Match   5.6%;   Score 124.5;   DB 8;   Length 1306;
Best Local Similarity   23.2%;   Pred. No. 1.5;
RESULT 558
ID   AEJ50087 standard; protein; 1306 AA.
DE   Saccharomyces cerevisiae stress-related protein (SRP) - SEQ ID 6.
PN   US2006137043-A1.
PD   22-JUN-2006.
PA   (BADI) BASF PLANT SCI GMBH.
Query Match   5.6%;   Score 124.5;   DB 10;   Length 1306;
Best Local Similarity   23.2%;   Pred. No. 1.5;
RESULT 559
ID   AAU01990 standard; protein; 169 AA.
DE   Gene #26 human secreted protein homologous amino acid sequence.
PN   WO200123598-A1.
PD   05-APR-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   5.6%;   Score 124;   DB 4;   Length 169;
Best Local Similarity   25.5%;   Pred. No. 0.089;
RESULT 560
ID   AAP60570 standard; protein; 844 AA.
DE   Sequence of the Falciparum Interspersed Repeat Antigen (FIRA).
PN   WO8601802-A.
PD   27-MAR-1986.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match   5.6%;   Score 124;   DB 1;   Length 844;
Best Local Similarity   25.4%;   Pred. No. 0.87;
RESULT 561
ID   ADO28932 standard; protein; 2590 AA.
DE   Mouse novel GPCR PGR17, SEQ ID NO.31.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
Query Match   5.6%;   Score 124;   DB 8;   Length 2590;

Best Local Similarity   22.6%;   Pred. No. 4.3;
RESULT 562
ID   AAR92803 standard; protein; 451 AA.
DE   Hepatitis A virus receptor.
PN   WO960376-A1.
PD   15-FEB-1996.
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match   5.6%;   Score 123.5;   DB 2;   Length 451;
Best Local Similarity   22.7%;   Pred. No. 0.39;
RESULT 563
ID   AEL57389 standard; protein; 465 AA.
DE   Mouse podocalypsin-like protein 1 precursor, SEQ ID NO: 1852.
PN   US2006216722-A1.
PD   28-SEP-2006.
PA   (BETS/) BETSHOLTZ C.
PA   (TRYG/) TRYGGVASON K.
PA   (TAKE/) TAKEMOTO M.
PA   (HELI/) HE L.
PA   (PATR/) PATRAKKAS J.
Query Match   5.6%;   Score 123.5;   DB 10;   Length 465;
Best Local Similarity   23.4%;   Pred. No. 0.41;
RESULT 564
ID   AAB98980 standard; protein; 503 AA.
DE   Murine PCLP1.
PN   WO200134797-A1.
PD   17-MAY-2001.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match   5.6%;   Score 123.5;   DB 4;   Length 503;
Best Local Similarity   23.4%;   Pred. No. 0.46;
RESULT 565
ID   ADV41989 standard; protein; 503 AA.
DE   Mouse podocalyxin protein.
PN   WO200410286-A2.
PD   16-DEC-2004.
PA   (UYBR-) UNIV BRITISH COLUMBIA.
Query Match   5.6%;   Score 123.5;   DB 9;   Length 503;
Best Local Similarity   23.4%;   Pred. No. 0.46;
RESULT 566
ID   AEL57387 standard; protein; 503 AA.
DE   Mouse podocalypsin-like protein 1 precursor, SEQ ID NO: 1850.
PN   US2006216722-A1.
PD   28-SEP-2006.
PA   (BETS/) BETSHOLTZ C.
PA   (TRYG/) TRYGGVASON K.
PA   (TAKE/) TAKEMOTO M.
PA   (HELI/) HE L.
PA   (PATR/) PATRAKKAS J.
Query Match   5.6%;   Score 123.5;   DB 10;   Length 503;
Best Local Similarity   23.4%;   Pred. No. 0.46;
RESULT 567
ID   ADC01840 standard; protein; 738 AA.
DE   C. albicans dimorphism-specific protein 2400.
PN   DE10142743-A1.
PD   13-MAR-2003.
PA   (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
Query Match   5.6%;   Score 123.5;   DB 7;   Length 738;
Best Local Similarity   19.5%;   Pred. No. 0.79;
RESULT 568
ID   ADD93398 standard; protein; 775 AA.
DE   Human lipid-associated molecule LIPAM-5 polypeptide.
PN   WO2003083081-A2.
PD   09-OCT-2003.
PA   (INCY-) INCYTE CORP.
Query Match   5.6%;   Score 123.5;   DB 7;   Length 775;
Best Local Similarity   20.0%;   Pred. No. 0.85;
RESULT 569
ID   ADQ26076 standard; protein; 793 AA.
DE   Low density lipoprotein receptor-related protein 8 #3.
PN   WO200456386-A2.
PD   08-JUL-2004.
PA   (UYLE-) RIJKSUNIV LEIDEN.
Query Match   5.6%;   Score 123.5;   DB 8;   Length 793;
Best Local Similarity   20.0%;   Pred. No. 0.88;

RESULT 570
ID   ADY19820 standard; protein; 793 AA.
DE   PRO polypeptide SEQ ID NO 5626.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
     Query Match   5.6%; Score 123.5; DB 9; Length 793;
     Best Local Similarity   20.0%; Pred. No. 0.88;

RESULT 571
ID   AAU91287 standard; protein; 804 AA.
DE   Human NOV5f protein.
PN   WO200216600-A2.
PD   28-FEB-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 5; Length 804;
     Best Local Similarity   20.0%; Pred. No. 0.89;

RESULT 572
ID   ADH71754 standard; protein; 804 AA.
DE   Human protein of the invention NOV28g SEQ ID NO:650.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 5; Length 804;
     Best Local Similarity   20.0%; Pred. No. 0.89;

RESULT 573
ID   ADD93402 standard; protein; 834 AA.
DE   Human lipid-associated molecule LIIPAM-9 polypeptide.
PN   WO2003083081-A2.
PD   09-OCT-2003.
PA   (INCY-) INCYTE CORP.
     Query Match   5.6%; Score 123.5; DB 7; Length 834;
     Best Local Similarity   20.0%; Pred. No. 0.94;

RESULT 574
ID   AAU91289 standard; protein; 847 AA.
DE   Human NOV5h protein.
PN   WO200216600-A2.
PD   28-FEB-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 5; Length 847;
     Best Local Similarity   20.0%; Pred. No. 0.96;

RESULT 575
ID   ADH71758 standard; protein; 847 AA.
DE   Human protein of the invention NOV28i SEQ ID NO:654.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 8; Length 847;
     Best Local Similarity   20.0%; Pred. No. 0.96;

RESULT 576
ID   AAU91288 standard; protein; 857 AA.
DE   Human NOV5g protein.
PN   WO200216600-A2.
PD   28-FEB-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 5; Length 857;
     Best Local Similarity   20.0%; Pred. No. 0.98;

RESULT 577
ID   ADH71756 standard; protein; 857 AA.
DE   Human protein of the invention NOV28h SEQ ID NO:652.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 8; Length 857;
     Best Local Similarity   20.0%; Pred. No. 0.98;

RESULT 578
ID   ADD93401 standard; protein; 904 AA.
DE   Human lipid-associated molecule LIIPAM-8 polypeptide.
PN   WO2003083081-A2.
PD   09-OCT-2003.
PA   (INCY-) INCYTE CORP.
     Query Match   5.6%; Score 123.5; DB 7; Length 904;
     Best Local Similarity   20.0%; Pred. No. 1.1;

RESULT 579
ID   ADH71742 standard; protein; 905 AA.
DE   Human protein of the invention NOV28a SEQ ID NO:638.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 8; Length 905;
     Best Local Similarity   20.0%; Pred. No. 1.1;

RESULT 580
ID   ADH71766 standard; protein; 905 AA.
DE   Human protein of the invention NOV28m SEQ ID NO:662.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 8; Length 905;
     Best Local Similarity   20.0%; Pred. No. 1.1;

RESULT 581
ID   ABP56838 standard; protein; 963 AA.
DE   Human apolipoprotein E receptor 2 protein SEQ ID NO:5.
PN   WO200299438-A2.
PD   12-DEC-2002.
PA   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PA   (UYAA-) UNIV AARHUS.
     Query Match   5.6%; Score 123.5; DB 6; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 582
ID   ADH71764 standard; protein; 963 AA.
DE   Human protein of the invention NOV281 SEQ ID NO:660.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 8; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 583
ID   ADI27185 standard; protein; 963 AA.
DE   Human LRP binding family protein #14.
PN   WO2003106657-A2.
PD   24-DEC-2003.
PA   (STOW-) STOWERS INST MEDICAL RES.
     Query Match   5.6%; Score 123.5; DB 8; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 584
ID   ADN00737 standard; protein; 963 AA.
DE   Human LDLR, SEQ ID 10.
PN   WO2004024881-A2.
PD   25-MAR-2004.
PA   (EXEL-) EXELIXIS INC.
     Query Match   5.6%; Score 123.5; DB 8; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 585
ID   ADO19504 standard; protein; 963 AA.
DE   Human PRO polypeptide #217.
PN   WO2004043361-A2.
PD   27-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.6%; Score 123.5; DB 8; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 586
ID   ADQ26074 standard; protein; 963 AA.
DE   Low density lipoprotein receptor-related protein 8 #1.
PN   WO2004056386-A2.
PD   08-JUL-2004.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match   5.6%; Score 123.5; DB 8; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 587
ID   ADY15958 standard; protein; 963 AA.
DE   PRO polypeptide SEQ ID NO 1764.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
     Query Match   5.6%; Score 123.5; DB 9; Length 963;
     Best Local Similarity   20.0%; Pred. No. 1.2;

RESULT 588

ID   ABP27418 standard; protein; 970 AA.
DE   Streptococcus polypeptide SEQ ID NO 4012.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match   5.6%; Score 123.5; DB 5; Length 970;
     Best Local Similarity 22.6%; Pred. No. 1.2;
RESULT 589
ID   AAU91285 standard; protein; 1012 AA.
DE   Human NOV5d protein.
PN   WO200216600-A2.
PD   28-FEB-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 5; Length 1012;
     Best Local Similarity 20.0%; Pred. No. 1.2;
RESULT 590
ID   ADH71750 standard; protein; 1012 AA.
DE   Human protein of the invention NOV28e SEQ ID NO:646.
PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123.5; DB 8; Length 1012;
     Best Local Similarity 20.0%; Pred. No. 1.2;
RESULT 591
ID   AAB11744 standard; protein; 150 AA.
DE   C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:18.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.6%; Score 123; DB 3; Length 150;
     Best Local Similarity 23.0%; Pred. No. 0.091;
RESULT 592
ID   ABJ04057 standard; protein; 150 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 18.
PN   WO200194631-A1.
PD   13-DEC-2001.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.6%; Score 123; DB 5; Length 150;
     Best Local Similarity 23.0%; Pred. No. 0.091;
RESULT 593
ID   AAB11734 standard; protein; 216 AA.
DE   Cryptosporidium parvum NINC isolate GP900, domain 2.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.6%; Score 123; DB 3; Length 216;
     Best Local Similarity 23.1%; Pred. No. 0.15;
RESULT 594
ID   AAW38336 standard; protein; 334 AA.
DE   Human kidney injury related molecule (KIM).
PN   WO9744460-A1.
PD   27-NOV-1997.
PA   (BIOJ) BIOGEN INC.
     Query Match   5.6%; Score 123; DB 2; Length 334;
     Best Local Similarity 23.1%; Pred. No. 0.28;
RESULT 595
ID   AAO26679 standard; protein; 334 AA.
DE   KIM-1 related protein, SEQ ID No 7.
PN   WO200298920-A1.
PD   12-DEC-2002.
PA   (BIOJ) BIOGEN INC.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   5.6%; Score 123; DB 3; Length 334;
     Best Local Similarity 25.0%; Pred. No. 0.28;
RESULT 596
ID   ADQ76696 standard; protein; 334 AA.
DE   Human kidney injury molecule-1 (KIM-1).
PN   WO200406041-A2.
PD   22-JUL-2004.
PA   (BIOG-) BIOGEN IDEC MA INC.
     Query Match   5.6%; Score 123; DB 8; Length 334;
     Best Local Similarity 23.1%; Pred. No. 0.28;

RESULT 597
ID   AD279369 standard; protein; 334 AA.
DE   Human kidney injury molecule-1(a) complete protein.
PN   US2005112117-A1.
PD   26-MAY-2005.
PA   (BAIL/) BAILLY V.
PA   (BONV/) BONVENTRE J.
     Query Match   5.6%; Score 123; DB 9; Length 334;
     Best Local Similarity 23.1%; Pred. No. 0.28;
RESULT 598
ID   ADB36618 standard; protein; 339 AA.
DE   Plasmid pCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.
PN   WO2003080856-A2.
PD   02-OCT-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123; DB 7; Length 339;
     Best Local Similarity 23.1%; Pred. No. 0.29;
RESULT 599
ID   ADB36592 standard; protein; 339 AA.
DE   Human NOV1a protein SEQ ID NO:2.
PN   WO2003080856-A2.
PD   02-OCT-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.6%; Score 123; DB 7; Length 339;
     Best Local Similarity 23.1%; Pred. No. 0.29;
RESULT 600
ID   ABC32061 standard; protein; 339 AA.
DE   Human CG57008-03 protein, SEQ ID NO: 6.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
     Query Match   5.6%; Score 123; DB 9; Length 339;
     Best Local Similarity 23.1%; Pred. No. 0.29;
RESULT 601
ID   AEK20430 standard; protein; 339 AA.
DE   Human KIM-1 polypeptide.
PN   WO2006094134-A2.
PD   08-SEP-2006.
PA   (BIOJ) BIOGEN IDEC MA INC.
     Query Match   5.6%; Score 123; DB 10; Length 339;
     Best Local Similarity 23.1%; Pred. No. 0.29;
RESULT 602
ID   ABR58582 standard; protein; 359 AA.
DE   Human cancer related protein SEQ ID NO:239.
PN   WO2003025138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   5.6%; Score 123; DB 6; Length 359;
     Best Local Similarity 23.1%; Pred. No. 0.31;
RESULT 603
ID   ABP70439 standard; protein; 359 AA.
DE   Amino acid sequence of human TIM-1 allele 1.
PN   WO2003002722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.6%; Score 123; DB 6; Length 359;
     Best Local Similarity 23.1%; Pred. No. 0.31;
RESULT 604
ID   ABP70438 standard; protein; 359 AA.
DE   Amino acid sequence of human TIM-1 allele 1.
PN   WO2003002722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.6%; Score 123; DB 6; Length 359;
     Best Local Similarity 23.1%; Pred. No. 0.31;
RESULT 605
ID   ABR48174 standard; protein; 359 AA.
DE   Human bladder cancer associated protein sequence SEQ ID NO:64.
PN   WO2003003906-A2.
PD   16-JAN-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.

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          Query Match          5.6%;   Score 123; DB 6;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 606
ID   AAO26680 standard; protein; 359 AA.
DE   KIM-1 related protein, SEQ ID No 8.
PN   WO200298920-A1.
PD   12-DEC-2002.
PA   (BIOJ ) GEN HOSPITAL CORP.
PA   (GEHO ) GEN HOSPITAL CORP.
          Query Match          5.6%;   Score 123; DB 6;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 607
ID   ADE36594 standard; protein; 359 AA.
DE   Human NOV1b protein SEQ ID NO:4.
PN   WO2003080856-A2.
PD   02-OCT-2003.
PA   (CURA-) CURAGEN CORP.
          Query Match          5.6%;   Score 123; DB 7;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 608
ID   ADN38984 standard; protein; 359 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
          Query Match          5.6%;   Score 123; DB 7;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 609
ID   ADQ76690 standard; protein; 359 AA.
DE   Human kidney injury molecule-1 (KIM-1).
PN   WO2004060041-A2.
PD   22-JUL-2004.
PA   (BIOG-) BIOGEN IDEC MA INC.
          Query Match          5.6%;   Score 123; DB 8;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 610
ID   ABR99971 standard; protein; 359 AA.
DE   HAVCR1 protein, SEQ ID 25.
PN   WO2005001092-A2.
PD   06-JAN-2005.
PA   (AMHP ) WYETH.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 611
ID   ADY98071 standard; protein; 359 AA.
DE   Human TIM-1 allele 1-encoded protein.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (DAND ) DANA FARBER CANCER INST INC.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 612
ID   ADY98073 standard; protein; 359 AA.
DE   Human TIM-1 allele 2-encoded protein.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
PA   (DAND ) DANA FARBER CANCER INST INC.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 613
ID   AD279370 standard; protein; 359 AA.
DE   Human kidney injury molecule-1(b) complete protein.
PN   US2005112117-A1.
PD   26-MAY-2005.
PA   (BAIL/) BAILLY V.
PA   (BONV/) BONVENTRE J.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 614
ID   AEC32091 standard; protein; 359 AA.
DE   Human CG57008-01-SNP P174L protein, SEQ ID NO: 36.

PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 615
ID   AEC33089 standard; protein; 359 AA.
DE   Human CG57008-01-SNP T202A protein, SEQ ID NO: 34.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 616
ID   AEC32057 standard; protein; 359 AA.
DE   Human CG57008-01 protein, SEQ ID NO: 2.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 617
ID   AEC32095 standard; protein; 359 AA.
DE   Human CG57008-01-SNP S51L protein, SEQ ID NO: 40.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 618
ID   AEC32097 standard; protein; 359 AA.
DE   Human CG57008-01-SNP A96V protein, SEQ ID NO: 42.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 619
ID   AED01583 standard; protein; 359 AA.
DE   Human tim-1 polypeptide.
PN   WO2005090573-A2.
PD   29-SEP-2005.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 620
ID   AED60515 standard; protein; 359 AA.
DE   Human TIM-1, allele 1, protein SEQ ID NO:23.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 621
ID   AED60517 standard; protein; 359 AA.
DE   Human TIM-1, allele 2, protein SEQ ID NO:25.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
          Query Match          5.6%;   Score 123; DB 9;   Length 359;
          Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 622
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ID   ABE19172 standard; protein; 359 AA.
DE   Human kidney-injury molecule 1 (KIM-1) protein, SEQ ID NO: 15.
PN   US2005265995-A1.
PD   01-DEC-2005.
PA   (TOML/) TOMLINSON S.
PA   (QUIG/) QUIGG R J.
     Query Match             5.6%;    Score 123; DB 9;  Length 359;
     Best Local Similarity   23.1%;   Pred. No. 0.31;
RESULT 623
ID   AEC32071 standard; protein; 362 AA.
DE   Human CG57008-08 protein, SEQ ID NO: 16.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
     Query Match             5.6%;    Score 123; DB 9;  Length 362;
     Best Local Similarity   23.1%;   Pred. No. 0.32;
RESULT 624
ID   AEC32069 standard; protein; 366 AA.
DE   Human CG57008-07 protein, SEQ ID NO: 14.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
     Query Match             5.6%;    Score 123; DB 9;  Length 366;
     Best Local Similarity   23.1%;   Pred. No. 0.32;
RESULT 625
ID   AB084406 standard; protein; 594 AA.
DE   Mouse cancer-associated protein MP7-023.1.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match             5.6%;    Score 123; DB 8;  Length 594;
     Best Local Similarity   27.2%;   Pred. No. 0.64;
RESULT 626
ID   ADD25508 standard; protein; 630 AA.
DE   Binding domain-immunoglobulin fusion protein-associated protein #31.
PN   US2003118592-A1.
PD   26-JUN-2003.
PA   (GENE-) GENECRAFT INC.
     Query Match             5.6%;    Score 123; DB 7;  Length 630;
     Best Local Similarity   22.1%;   Pred. No. 0.7;
RESULT 627
ID   ABB60403 standard; protein; 2112 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #13.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 2112;
     Best Local Similarity   26.2%;   Pred. No. 0.61;
RESULT 628
ID   ABU53153 standard; protein; 540 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #10.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.6%;    Score 123; DB 4;  Length 540;
     Best Local Similarity   31.4%;   Pred. No. 3.9;
RESULT 629
ID   ABU53150 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #9.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 630
ID   ABU53149 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #
PN   WO200112659-A2.
PD   22-FEB-2001.

PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 631
ID   ABU53151 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #11.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 632
ID   ABU53145 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #5.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 633
ID   ABU53148 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #8.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 634
ID   ABU53147 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #7.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 635
ID   ABU53146 standard; protein; 717 AA.
DE   Human testes-derived DKFZphtes3_2all homologue #6.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 717;
     Best Local Similarity   26.2%;   Pred. No. 0.92;
RESULT 636
ID   AAU37120 standard; protein; 2344 AA.
DE   Staphylococcus aureus cellular proliferation protein #1290.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELiTRA PHARM INC.
     Query Match             5.5%;    Score 122.5; DB 4;  Length 2344;
     Best Local Similarity   20.6%;   Pred. No. 4.9;
RESULT 637
ID   AEC32093 standard; protein; 359 AA.
DE   Human CG57008-01-SNP V138I protein, SEQ ID NO: 38.
PN   US2005197292-A1.
PD   08-SEP-2005.
PA   (SMIT/) SMITHSON G.
PA   (MESR/) MESRI M.
PA   (STAR/) STARLING G.
     Query Match             5.5%;    Score 122; DB 9;  Length 359;
     Best Local Similarity   22.8%;   Pred. No. 0.38;
RESULT 638
ID   ADB64343 standard; protein; 619 AA.
DE   Human protein encoded by clone FCBBF30125460.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match             5.5%;    Score 122; DB 7;  Length 619;
     Best Local Similarity   22.6%;   Pred. No. 0.82;
RESULT 639
ID   ABB61085 standard; protein; 724 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 10047.
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PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             5.5%;  Score 122;  DB 4;  Length 724;
     Best Local Similarity  19.8%;  Pred. No. 1;
RESULT 640
ID   ABB59201 standard; protein; 746 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 4395.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             5.5%;  Score 122;  DB 4;  Length 746;
     Best Local Similarity  24.7%;  Pred. No. 1.1;
RESULT 641
ID   ADG39831 standard; protein; 1019 AA.
DE   Protein similar to human NOV6 #4.
PN   US2003203843-A1.
PD   30-OCT-2003.
PA   (PENA/) PENA C E A.
PA   (GUOX/) GUO X.
PA   (SHIM/) SHIMKETS R A.
PA   (PADI/) PADIGARU M.
PA   (KEKU/) KEKUDA R.
PA   (SPYT/) SPYTEK K A.
PA   (MEHR/) MEHRABAN F.
PA   (TOPP/) TOPPER J N.
PA   (MALY/) MALYANKAR U M.
PA   (WASS/) WASSERMAN S M.
PA   (EDIN/) EDINGER S R.
PA   (SMIT/) SMITHSON G.
PA   (GUNT/) GUNTHER E.
PA   (KOMU/) KOMUVES L.
     Query Match             5.5%;  Score 122;  DB 7;  Length 1019;
     Best Local Similarity  23.3%;  Pred. No. 1.7;
RESULT 642
ID   ABB59325 standard; protein; 1486 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 4767.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             5.5%;  Score 122;  DB 4;  Length 1486;
     Best Local Similarity  20.1%;  Pred. No. 2.8;
RESULT 643
ID   ABB69419 standard; protein; 1976 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 35049.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             5.5%;  Score 122;  DB 4;  Length 1976;
     Best Local Similarity  21.3%;  Pred. No. 4.3;
RESULT 644
ID   AAB11729 standard; protein; 216 AA.
DE   Cryptosporidium parvum Iowa isolate GP900, domain 2.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match             5.5%;  Score 121.5;  DB 3;  Length 216;
     Best Local Similarity  25.5%;  Pred. No. 0.2;
RESULT 645
ID   ABJ04047 standard; protein; 216 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 8.
PN   WO200194631-A1.
PD   13-DEC-2001.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match             5.5%;  Score 121.5;  DB 5;  Length 216;
     Best Local Similarity  25.5%;  Pred. No. 0.2;
RESULT 646
ID   AAB80639 standard; protein; 274 AA.
DE   Environmental stress tolerant protein SEQ ID 64.
PN   WO200106006-A1.
PD   25-JAN-2001.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
     Query Match             5.5%;  Score 121.5;  DB 4;  Length 274;
     Best Local Similarity  30.0%;  Pred. No. 0.28;
RESULT 647
ID   ADC31035 standard; protein; 679 AA.
DE   Human novel polypeptide sequence, SEQ ID NO:1117.
PN   WO200329271-A2.
PD   10-APR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match             5.5%;  Score 121.5;  DB 7;  Length 679;
     Best Local Similarity  22.4%;  Pred. No. 1.
RESULT 648
ID   AEE72766 standard; protein; 702 AA.
DE   Novel human protein amino acid sequence - SEQ ID 28.
PN   JP2003116575-A.
PD   22-APR-2003.
PA   (KAZU-) ZH KAZUSA DNA KENKYUSHO.
     Query Match             5.5%;  Score 121.5;  DB 7;  Length 702;
     Best Local Similarity  22.4%;  Pred. No. 1.1;
RESULT 649
ID   AD48633 standard; protein; 736 AA.
DE   Oil-associated gene related protein #133.
PN   US2004025202-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.
PA   (LEDE/) LEDEAUX J R.
PA   (ROGE/) ROGERS J A.
     Query Match             5.5%;  Score 121.5;  DB 8;  Length 736;
     Best Local Similarity  24.5%;  Pred. No. 1.2;
RESULT 650
ID   ADN19282 standard; protein; 1041 AA.
DE   Bacterial polypeptide #1935.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match             5.5%;  Score 121.5;  DB 8;  Length 1041;
     Best Local Similarity  23.2%;  Pred. No. 1.9;
RESULT 651
ID   ABU02253 standard; protein; 4776 AA.
DE   S. pneumoniae type 4 strain protein from coding region #1831.
PN   WO200277021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match             5.5%;  Score 121.5;  DB 6;  Length 4776;
     Best Local Similarity  22.7%;  Pred. No. 16;
RESULT 652
ID   ABU45754 standard; protein; 4776 AA.
DE   Protein encoded by Prokaryotic essential gene #31281.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.5%;  Score 121.5;  DB 6;  Length 4776;
     Best Local Similarity  22.7%;  Pred. No. 16;
RESULT 653
ID   ADM92212 standard; protein; 4776 AA.
DE   S pneumoniae antigenic protein sequence SeqID409.
PN   WO200420609-A2.
PD   11-MAR-2004.
PA   (TUFT ) UNIV TUFTS.
     Query Match             5.5%;  Score 121.5;  DB 8;  Length 4776;
     Best Local Similarity  22.7%;  Pred. No. 16;
RESULT 654
ID   ADT50139 standard; protein; 4776 AA.
DE   S_pneumoniae hyperimmune serum reactive antigenic protein Seq 217.
PN   WO200409209-A3.
PD   28-OCT-2004.
PA   (INTE-) INTERCELL AG.
     Query Match             5.5%;  Score 121.5;  DB 8;  Length 4776;
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Best Local Similarity 22.7%; Pred. No. 16;
RESULT 655
ID ABP70441 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 4.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.5%; Score 121; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 0.46;
RESULT 656
ID ADY98077 standard; protein; 359 AA.
DE Human TIM-1 allele 4-encoded protein.
PN WO2005027854-A2.
PD 31-MAR-2005.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 5.5%; Score 121; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 0.46;
RESULT 657
ID ABD60521 standard; protein; 359 AA.
DE Human TIM-1, allele 4, protein SEQ ID NO:29.
PN WO2005097211-A2.
PD 20-OCT-2005.
PA (TELO-) TELOS PHARM INC.
Query Match 5.5%; Score 121; DB 9; Length 359;
Best Local Similarity 23.1%; Pred. No. 0.46;
RESULT 658
ID AEG97388 standard; protein; 714 AA.
DE C. albicans cell wall protein RBT1 SEQ ID NO 157.
PN WO2006036817-A2.
PD 06-APR-2006.
PA (MICR-) MICROBIA INC.
Query Match 5.5%; Score 121; DB 10; Length 714;
Best Local Similarity 22.1%; Pred. No. 1.2;
RESULT 659
ID AAY05477 standard; protein; 750 AA.
DE C. albicans Rbt1 protein sequence.
PN WO9918115-A1.
PD 15-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.5%; Score 121; DB 2; Length 750;
Best Local Similarity 22.1%; Pred. No. 1.3;
RESULT 660
ID AAY59288 standard; protein; 957 AA.
DE Human MUC11 polypeptide.
PN WO200004142-A1.
PD 27-JAN-2000.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Query Match 5.5%; Score 121; DB 3; Length 957;
Best Local Similarity 24.3%; Pred. No. 1.8;
RESULT 661
ID AAM24513 standard; protein; 957 AA.
DE C900P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 121; DB 4; Length 957;
Best Local Similarity 24.3%; Pred. No. 1.8;
RESULT 662
ID ABP55362 standard; protein; 957 AA.
DE Human colon tumour protein for clone C900P SEQ ID NO:1065.
PN WO200283070-A2.
PD 24-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 121; DB 6; Length 957;
Best Local Similarity 24.3%; Pred. No. 1.8;
RESULT 663
ID ADD47260 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12954.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
Query Match 5.5%; Score 121; DB 7; Length 957;
Best Local Similarity 22.1%; Pred. No. 1.8;
RESULT 664
ID ADE58049 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3917.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.5%; Score 121; DB 7; Length 957;
Best Local Similarity 22.1%; Pred. No. 1.8;
RESULT 665
ID ADD47264 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12958.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.5%; Score 121; DB 7; Length 957;
Best Local Similarity 22.1%; Pred. No. 1.8;
RESULT 666
ID ADE58045 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3913.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.5%; Score 121; DB 7; Length 957;
Best Local Similarity 22.1%; Pred. No. 1.8;
RESULT 667
ID AEA20406 standard; protein; 1004 AA.
DE Novel human polypeptide SEQ ID NO 1100.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 5.5%; Score 121; DB 9; Length 1004;
Best Local Similarity 24.3%; Pred. No. 2.
RESULT 668
ID AEA20405 standard; protein; 1032 AA.
DE Novel human polypeptide SEQ ID NO 1099.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 5.5%; Score 121; DB 9; Length 1032;
Best Local Similarity 24.3%; Pred. No. 2.
RESULT 669
ID ABG08332 standard; protein; 1045 AA.
DE Novel human diagnostic protein #8323.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 121; DB 4; Length 1045;
Best Local Similarity 21.4%; Pred. No. 2.1.
RESULT 670
ID AAB40945 standard; protein; 1532 AA.
DE Human ORFX ORF709 polypeptide sequence SEQ ID NO:1418.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.5%; Score 121; DB 3; Length 1532;
Best Local Similarity 21.4%; Pred. No. 3.6.
RESULT 671
ID ABG93090 standard; protein; 1796 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 138.
PN WO200264766-A1.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.5%; Score 121; DB 5; Length 1796;
Best Local Similarity 26.0%; Pred. No. 4.5.
RESULT 672
ID ADH32883 standard; protein; 1841 AA.
DE Yeast smORF635-encoded polypeptide, SEQ ID NO:1341.

PN   WO200268693-A2.
PD   06-SEP-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.5%; Score 121; DB 5; Length 1841;
     Best Local Similarity 26.0%; Pred. No. 4.6;
RESULT 673
ID   ABP70443 standard; protein; 364 AA.
DE   Amino acid sequence of human TIM-1 allele 6.
PN   WO2003302722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.5%; Score 120.5; DB 6; Length 364;
     Best Local Similarity 23.5%; Pred. No. 0.51;
RESULT 674
ID   ADY98081 standard; protein; 364 AA.
DE   Human TIM-1 allele 5-encoded protein.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.5%; Score 120.5; DB 9; Length 364;
     Best Local Similarity 23.5%; Pred. No. 0.51;
RESULT 675
ID   AED60525 standard; protein; 364 AA.
DE   Human TIM-1, allele 6, protein SEQ ID NO:33.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
     (DAND) DANA FARBER CANCER INST INC.
     Query Match   5.5%; Score 120.5; DB 9; Length 364;
     Best Local Similarity 23.5%; Pred. No. 0.51;
RESULT 676
ID   AAM16015 standard; protein; 386 AA.
DE   Peptide #2449 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 677
ID   ABB35008 standard; peptide; 386 AA.
DE   Peptide #2514 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 678
ID   AAM28516 standard; protein; 386 AA.
DE   Peptide #2553 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 679
ID   ABB29832 standard; peptide; 386 AA.
DE   Peptide #2483 encoded by breast cell single exon nucleic acid probe.
PN   WO200157271-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 680
ID   ABB20422 standard; protein; 386 AA.
DE   Protein #2421 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 681
ID   AAM68195 standard; protein; 386 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 28501.

PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 682
ID   AAM55821 standard; protein; 386 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 27926.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 683
ID   ABG49844 standard; peptide; 386 AA.
DE   Human liver peptide, SEQ ID No 28492.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 684
ID   AAM03749 standard; protein; 386 AA.
DE   Peptide #2431 encoded by probe for measuring breast gene expression.
PN   WO200157270-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.5%; Score 120.5; DB 4; Length 386;
     Best Local Similarity 30.3%; Pred. No. 0.56;
RESULT 685
ID   AAR67652 standard; protein; 409 AA.
DE   Glucomylase.
PN   JP06303984-A.
PD   01-NOV-1994.
PA   (NISB) JAPAN TOBACCO INC.
     Query Match   5.5%; Score 120.5; DB 2; Length 409;
     Best Local Similarity 21.3%; Pred. No. 0.61;
RESULT 686
ID   AEB40437 standard; protein; 429 AA.
DE   L. pneumophila protein SEQ ID NO 4769.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
     (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
     (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
     (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   5.5%; Score 120.5; DB 9; Length 429;
     Best Local Similarity 20.2%; Pred. No. 0.65;
RESULT 687
ID   ADH71760 standard; protein; 775 AA.
DE   Human protein of the invention NOV28j SEQ ID NO:656.
PN   WO200310215-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.5%; Score 120.5; DB 8; Length 775;
     Best Local Similarity 20.4%; Pred. No. 1.5;
RESULT 688
ID   AAU91290 standard; protein; 905 AA.
DE   Human NOV5i protein.
PN   WO200216600-A2.
PD   28-FEB-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.5%; Score 120.5; DB 5; Length 905;
     Best Local Similarity 19.8%; Pred. No. 1.9;
RESULT 689
ID   ABB71090 standard; protein; 916 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40062.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKB) PE CORP NY.
     Query Match   5.5%; Score 120.5; DB 4; Length 916;
     Best Local Similarity 22.9%; Pred. No. 1.9;
RESULT 690

ID   AAP60723 standard; protein; 918 AA.
DE   Sequence of extracellular amylo-alpha-1,4-glucosidase (AMG) precursor.
PN   WO8603778-A.
PD   03-JUL-1986.
PA   (BREW-) BREWING RES FOUND.
PA   (TUBB/) TUBB R S.
PA   (CLLT) CELLTECH LTD.
Query Match   5.5%;   Score 120.5; DB 1; Length 918;
Best Local Similarity   21.3%;   Pred. No. 1.9;
RESULT 691
ID   ADS43858 standard; protein; 1169 AA.
DE   Bacterial polypeptide #22288.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match   5.5%;   Score 120.5; DB 8; Length 1169;
Best Local Similarity   19.2%;   Pred. No. 2.7;
RESULT 692
ID   ABU18239 standard; protein; 1194 AA.
DE   Protein encoded by Prokaryotic essential gene #3766.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.5%;   Score 120.5; DB 6; Length 1194;
Best Local Similarity   20.4%;   Pred. No. 2.8;
RESULT 693
ID   ADU69631 standard; protein; 1310 AA.
DE   S agalactiae hyperimmune serum reactive antigen seqid 326.
PN   WO2004099242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
Query Match   5.5%;   Score 120.5; DB 8; Length 1310;
Best Local Similarity   22.9%;   Pred. No. 3.2;
RESULT 694
ID   ADV89548 standard; protein; 1310 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 1942.
PN   FR2824074-A1.
PD   31-OCT-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
Query Match   5.5%;   Score 120.5; DB 8; Length 1310;
Best Local Similarity   22.9%;   Pred. No. 3.2;
RESULT 695
ID   ADV80801 standard; protein; 1310 AA.
DE   Streptococcus agalactiae protein, SEQ ID 1942.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
Query Match   5.5%;   Score 120.5; DB 8; Length 1310;
Best Local Similarity   22.9%;   Pred. No. 3.2;
RESULT 696
ID   ADV82959 standard; protein; 1310 AA.
DE   Streptococcus agalactiae protein, SEQ ID 4100.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
Query Match   5.5%;   Score 120.5; DB 8; Length 1310;
Best Local Similarity   22.9%;   Pred. No. 3.2;
RESULT 697
ID   ABM85586 standard; protein; 410 AA.
DE   Mouse protein sequence mCP10498.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
Query Match   5.4%;   Score 120; DB 7; Length 410;
Best Local Similarity   27.6%;   Pred. No. 0.67;
RESULT 698

ID   AAM39963 standard; protein; 540 AA.
DE   Human polypeptide SEQ ID NO 3108.
PN   WO20015312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   5.4%;   Score 120; DB 4; Length 540;
Best Local Similarity   21.5%;   Pred. No. 0.99;
RESULT 699
ID   ABP61508 standard; protein; 540 AA.
DE   Human NF-kB activating protein SEQ ID NO 170.
PN   WO200253737-A1.
PD   11-JUL-2002.
PA   (ASAH) ASAHI KASEI KOGYO KK.
Query Match   5.4%;   Score 120; DB 5; Length 540;
Best Local Similarity   21.5%;   Pred. No. 0.99;
RESULT 700
ID   ADC37213 standard; protein; 540 AA.
DE   Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 46.
PN   WO2003048202-A2.
PD   12-JUN-2003.
PA   (ASAH) ASAHI KASEI KK.
Query Match   5.4%;   Score 120; DB 7; Length 540;
Best Local Similarity   21.5%;   Pred. No. 0.99;
RESULT 701
ID   ADR89526 standard; protein; 540 AA.
DE   Apoptosis-inducing protein, SEQ ID 50.
PN   WO200478112-A2.
PD   16-SEP-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match   5.4%;   Score 120; DB 8; Length 540;
Best Local Similarity   21.5%;   Pred. No. 0.99;
RESULT 702
ID   ADV99534 standard; protein; 540 AA.
DE   Human membrane -bound stimulator of endothelial proliferation, SEP #2.
PN   WO2004111085-A1.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
Query Match   5.4%;   Score 120; DB 9; Length 540;
Best Local Similarity   21.5%;   Pred. No. 0.99;
RESULT 703
ID   ADW43168 standard; protein; 540 AA.
DE   Human membrane-bound angiogenic factor SEP protein - SEQ ID 6.
PN   WO2004111088-A2.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
Query Match   5.4%;   Score 120; DB 9; Length 540;
Best Local Similarity   21.5%;   Pred. No. 0.99;
RESULT 704
ID   ABP69770 standard; protein; 957 AA.
DE   Human polypeptide SEQ ID NO 1817.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSE-) HYSEQ INC.
Query Match   5.4%;   Score 120; DB 5; Length 957;
Best Local Similarity   23.9%;   Pred. No. 2.2;
RESULT 705
ID   AAU84374 standard; protein; 957 AA.
DE   Novel human secreted or membrane-associated protein #13.
PN   WO200204600-A2.
PD   17-JAN-2002.
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
PA   (GLAX) GLAXO GROUP LTD.
Query Match   5.4%;   Score 120; DB 5; Length 957;
Best Local Similarity   23.9%;   Pred. No. 2.2;
RESULT 706
ID   ADJ69195 standard; protein; 991 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1001.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
Query Match   5.4%;   Score 120; DB 7; Length 991;

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Best Local Similarity   23.9%;   Pred. No. 2.3;
RESULT 707
ID   ADQ29696 standard; protein; 1217 AA.
DE   Human colorectal cancer-associated protein #51.
PN   EP1439393-A2.
PD   21-JUL-2004.
PA   (FARB ) BAYER HEALTHCARE LLC.
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match        5.4%;   Score 120; DB 8;   Length 1217;
Best Local Similarity   21.8%;   Pred. No. 3.1;
RESULT 708
ID   AEF70008 standard; protein; 1217 AA.
DE   Colorectal cancer-associated marker protein SEQ ID NO:186.
PN   WO2006015047-A2.
PD   09-FEB-2006.
PA   (FARB ) BAYER HEALTHCARE LLC.
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match        5.4%;   Score 120; DB 10;  Length 1217;
Best Local Similarity   21.8%;   Pred. No. 3.1;
RESULT 709
ID   ADR18921 standard; protein; 1569 AA.
DE   Human mucin glycoprotein, MUC6.
PN   WO2004069136-A2.
PD   19-AUG-2004.
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match        5.4%;   Score 120; DB 8;   Length 1569;
Best Local Similarity   24.7%;   Pred. No. 4.5;
RESULT 710
ID   ABG74692 standard; protein; 1595 AA.
DE   Human CGDD protein 1925714CD1 SEQ ID 18.
PN   WO2003014322-A2.
PD   20-FEB-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match        5.4%;   Score 120; DB 6;   Length 1595;
Best Local Similarity   23.9%;   Pred. No. 4.6;
RESULT 711
ID   ABB88995 standard; protein; 230 AA.
DE   Babesia microti antigen BM61.
PN   WO200185947-A2.
PD   15-NOV-2001.
PA   (CORI-) CORIXA CORP.
Query Match        5.4%;   Score 119.5; DB 5;   Length 230;
Best Local Similarity   27.3%;   Pred. No. 0.32;
RESULT 712
ID   ABP64688 standard; protein; 465 AA.
DE   Human protein SEQ ID 348.
PN   WO200259260-A2.
PD   01-AUG-2002.
PA   (HYSE-) HYSEQ INC.
Query Match        5.4%;   Score 119.5; DB 5;   Length 465;
Best Local Similarity   24.9%;   Pred. No. 0.88;
RESULT 713
ID   AAM93404 standard; protein; 470 AA.
DE   Human polypeptide, SEQ ID NO: 3008.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match        5.4%;   Score 119.5; DB 4;   Length 470;
Best Local Similarity   25.4%;   Pred. No. 0.89;
RESULT 714
ID   AAM93679 standard; protein; 470 AA.
DE   Human polypeptide, SEQ ID NO: 3572.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match        5.4%;   Score 119.5; DB 4;   Length 470;
Best Local Similarity   25.4%;   Pred. No. 0.89;
RESULT 715
ID   AAB20327 standard; protein; 470 AA.
DE   Human protein phosphatase and kinase protein-6.
PN   WO200120004-A2.
PD   22-MAR-2001.
PA   (INCY-) INCYTE GENOMICS INC.

Query Match        5.4%;   Score 119.5; DB 4;   Length 470;
Best Local Similarity   25.4%;   Pred. No. 0.89;
RESULT 716
ID   AAM38987 standard; protein; 470 AA.
DE   Human polypeptide SEQ ID NO 2132.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
Query Match        5.4%;   Score 119.5; DB 4;   Length 470;
Best Local Similarity   24.7%;   Pred. No. 0.89;
RESULT 717
ID   ADL31539 standard; protein; 470 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3572.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match        5.4%;   Score 119.5; DB 8;   Length 470;
Best Local Similarity   25.4%;   Pred. No. 0.89;
RESULT 718
ID   ADL30975 standard; protein; 470 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3008.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match        5.4%;   Score 119.5; DB 8;   Length 470;
Best Local Similarity   25.4%;   Pred. No. 0.89;
RESULT 719
ID   ADX91809 standard; protein; 473 AA.
DE   Plant full length insert polypeptide seqid 54473.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match        5.4%;   Score 119.5; DB 8;   Length 473;
Best Local Similarity   25.4%;   Pred. No. 0.9;
RESULT 720
ID   ADX91849 standard; protein; 473 AA.
DE   Plant full length insert polypeptide seqid 54513.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match        5.4%;   Score 119.5; DB 8;   Length 473;
Best Local Similarity   25.4%;   Pred. No. 0.9;
RESULT 721
ID   ABO58564 standard; protein; 800 AA.
DE   Human genome derived single exon protein #4798.
PN   US200319704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
Query Match        5.4%;   Score 119.5; DB 8;   Length 800;
Best Local Similarity   26.3%;   Pred. No. 1.9;
RESULT 722
ID   ABB58990 standard; protein; 801 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 3762.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PKE ) PE CORP NY.
Query Match        5.4%;   Score 119.5; DB 4;   Length 801;
Best Local Similarity   22.4%;   Pred. No. 1.9;
RESULT 723
ID   AEC60057 standard; protein; 6995 AA.
DE   Human mucin 16 (MUC16).
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PN WO2005081711-A2.
PD 09-SEP-2005.
PA (SEAT-) SEATTLE GENETICS INC.
    Query Match   5.4%; Score 119.5; DB 9; Length 6995;
    Best Local Similarity 22.5%; Pred. No. 41;
RESULT 724
ID AEL74820 standard; protein; 6995 AA.
DE Cancer-associated antigen MUC16 fragment SEQ ID NO 44.
PN WO200106912-A1.
PD 12-OCT-2006.
PA (CHUS) CHUGAI SEIYAKU KK.
    Query Match   5.4%; Score 119.5; DB 10; Length 6995;
    Best Local Similarity 22.5%; Pred. No. 41;
RESULT 725
ID AAB11741 standard; protein; 138 AA.
DE C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:15.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.4%; Score 119; DB 3; Length 138;
    Best Local Similarity 26.5%; Pred. No. 0.17;
RESULT 726
ID ABJ04054 standard; protein; 138 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 15.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.4%; Score 119; DB 5; Length 138;
    Best Local Similarity 26.5%; Pred. No. 0.17;
RESULT 727
ID ADT58460 standard; protein; 210 AA.
DE Plant polypeptide, SEQ ID 8537.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
    Query Match   5.4%; Score 119; DB 8; Length 210;
    Best Local Similarity 26.5%; Pred. No. 0.31;
RESULT 728
ID AEJ97893 standard; protein; 475 AA.
DE Human MUC1 full length protein.
PN WO2006088906-A2.
PD 24-AUG-2006.
PA (DAND) DANA FARBER CANCER INST INC.
    Query Match   5.4%; Score 119; DB 10; Length 475;
    Best Local Similarity 25.4%; Pred. No. 0.99;
RESULT 729
ID ABP64687 standard; protein; 560 AA.
DE Human protein SEQ ID 347.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
    Query Match   5.4%; Score 119; DB 5; Length 560;
    Best Local Similarity 20.8%; Pred. No. 1.3;
RESULT 730
ID AAE01114 standard; protein; 595 AA.
DE Human gene 1 encoded secreted protein HBINK72, SEQ ID NO:28.
PN WO200134799-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   5.4%; Score 119; DB 4; Length 595;
    Best Local Similarity 20.8%; Pred. No. 1.4;
RESULT 731
ID ABG64591 standard; protein; 595 AA.
DE Human albumin fusion protein #1266.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   5.4%; Score 119; DB 5; Length 595;
    Best Local Similarity 20.8%; Pred. No. 1.4;
RESULT 732
ID ADL77858 standard; protein; 595 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1340.
PN US2004010134-A1.

PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
    Query Match   5.4%; Score 119; DB 8; Length 595;
    Best Local Similarity 20.8%; Pred. No. 1.4;
RESULT 733
ID AEH08132 standard; protein; 595 AA.
DE Therapeutic protein HBINK72, SEQ ID 1340.
PN US2006084794-A1.
PD 20-APR-2006.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   5.4%; Score 119; DB 10; Length 595;
    Best Local Similarity 20.8%; Pred. No. 1.4;
RESULT 734
ID AEG97331 standard; protein; 601 AA.
DE C. albicans hyphal growth inhibitor RFG1 SEQ ID NO 100.
PN WO2006035817-A2.
PD 06-APR-2006.
PA (MICR-) MICROBIA INC.
    Query Match   5.4%; Score 119; DB 10; Length 601;
    Best Local Similarity 20.0%; Pred. No. 1.4;
RESULT 735
ID ADI27184 standard; protein; 996 AA.
DE Mouse LRP binding family protein #20.
PN WO200310657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
    Query Match   5.4%; Score 119; DB 8; Length 996;
    Best Local Similarity 22.2%; Pred. No. 2.8;
RESULT 736
ID ABU54710 standard; protein; 1784 AA.
DE Human CA125 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
    Query Match   5.4%; Score 119; DB 6; Length 1784;
    Best Local Similarity 24.1%; Pred. No. 6.5;
RESULT 737
ID ABU54858 standard; protein; 1794 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
    Query Match   5.4%; Score 119; DB 6; Length 1794;
    Best Local Similarity 24.1%; Pred. No. 6.5;
RESULT 738
ID ABU54707 standard; protein; 1821 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
    Query Match   5.4%; Score 119; DB 6; Length 1821;
    Best Local Similarity 24.1%; Pred. No. 6.7;
RESULT 739
ID ADJ66747 standard; protein; 2234 AA.
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
PN WO200405470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
    Query Match   5.4%; Score 119; DB 8; Length 2234;
    Best Local Similarity 24.1%; Pred. No. 8.9;
RESULT 740
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
    Query Match   5.4%; Score 119; DB 6; Length 5877;
    Best Local Similarity 20.9%; Pred. No. 35;
RESULT 741
ID ABU54721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.

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PD  24-OCT-2002.
PA  (UYAR-) UNIV ARKANSAS.
    Query Match      5.4%;  Score 119; DB 6;  Length 11721;
    Best Local Similarity   24.1%;  Pred. No. 94;
RESULT 742
ID  ABB88979 standard; protein; 222 AA.
DE  Babesia microti antigen BM61.
PN  WO200185947-A2.
PD  15-NOV-2001.
PA  (CORI-) CORIXA CORP.
    Query Match      5.4%;  Score 118.5; DB 5;  Length 222;
    Best Local Similarity   28.3%;  Pred. No. 0.37;
RESULT 743
ID  ADE06068 standard; protein; 222 AA.
DE  BMNI-related polypeptide #41.
PN  US2003109689-A1.
PD  12-JUN-2003.
PA  (REED/) REED S G.
PA  (LODE/) LODES M J.
PA  (HOUG/) HOUGHTON R L.
PA  (SLEA/) SLEATH P R.
PA  (MCNE/) MCNEILL P D.
PA  (HOME/) HOMER M J.
PA  (SECR/) SECRIST H.
    Query Match      5.4%;  Score 118.5; DB 7;  Length 222;
    Best Local Similarity   28.3%;  Pred. No. 0.37;
RESULT 744
ID  ADE06123 standard; protein; 230 AA.
DE  BMNI-related polypeptide #57.
PN  US2003109689-A1.
PD  12-JUN-2003.
PA  (REED/) REED S G.
PA  (LODE/) LODES M J.
PA  (HOUG/) HOUGHTON R L.
PA  (SLEA/) SLEATH P R.
PA  (MCNE/) MCNEILL P D.
PA  (HOME/) HOMER M J.
PA  (SECR/) SECRIST H.
    Query Match      5.4%;  Score 118.5; DB 7;  Length 230;
    Best Local Similarity   28.3%;  Pred. No. 0.39;
RESULT 745
ID  ADI57779 standard; protein; 379 AA.
DE  Human breast specific protein (BSP) #56.
PN  WO2003106648-A2.
PD  24-DEC-2003.
PA  (DIAD-) DIADEXUS INC.
    Query Match      5.4%;  Score 118.5; DB 8;  Length 379;
    Best Local Similarity   26.3%;  Pred. No. 0.79;
RESULT 746
ID  ABM80527 standard; protein; 429 AA.
DE  Tumour-associated antigenic target (TAT) polypeptide PRO81088, SEQ:1339.
PN  WO2004030615-A2.
PD  15-APR-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      5.4%;  Score 118.5; DB 8;  Length 429;
    Best Local Similarity   21.6%;  Pred. No. 0.95;
RESULT 747
ID  ADX83214 standard; protein; 429 AA.
DE  Human TEG37 polypeptide SEQ ID NO 96.
PN  WO2005014818-A1.
PD  17-FEB-2005.
PA  (PERS-) PERSEUS PROTEOMICS INC.
PA  (CHUS ) CHUGAI SEIYAKU KK.
PA  (ABUR/) ABURATANI H.
    Query Match      5.4%;  Score 118.5; DB 9;  Length 429;
    Best Local Similarity   21.6%;  Pred. No. 0.95;
RESULT 748
ID  ABP65644 standard; protein; 483 AA.
DE  Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:388.
PN  EP1227152-A1.
PD  31-JUL-2002.
PA  (NEST ) SOC PROD NESTLE SA.
    Query Match      5.4%;  Score 118.5; DB 5;  Length 483;


    Best Local Similarity   22.3%;  Pred. No. 1.1;
RESULT 749
ID  AAR89927 standard; protein; 521 AA.
DE  A. cellulolyticus E1 endoglucanase.
PN  WO9602551-A1.
PD  01-FEB-1996.
PA  (MIDE ) MIDWEST RES INST.
    Query Match      5.4%;  Score 118.5; DB 2;  Length 521;
    Best Local Similarity   24.1%;  Pred. No. 1.2;
RESULT 750
ID  AAB48787 standard; protein; 521 AA.
DE  Acidothermus cellulolyticus E1 endoglucanase mutant, Y82R.
PN  WO200070031-A1.
PD  23-NOV-2000.
PA  (MIDE ) MIDWEST RES INST.
    Query Match      5.4%;  Score 118.5; DB 4;  Length 521;
    Best Local Similarity   24.1%;  Pred. No. 1.2;
RESULT 751
ID  AAB48786 standard; protein; 521 AA.
DE  Acidothermus cellulolyticus E1 endoglucanase mutant, W42R.
PN  WO200070031-A1.
PD  23-NOV-2000.
PA  (MIDE ) MIDWEST RES INST.
    Query Match      5.4%;  Score 118.5; DB 4;  Length 521;
    Best Local Similarity   24.1%;  Pred. No. 1.2;
RESULT 752
ID  AAB48788 standard; protein; 521 AA.
DE  Acidothermus cellulolyticus E1 endoglucanase mutant, Y245G.
PN  WO200070031-A1.
PD  23-NOV-2000.
PA  (MIDE ) MIDWEST RES INST.
    Query Match      5.4%;  Score 118.5; DB 4;  Length 521;
    Best Local Similarity   24.1%;  Pred. No. 1.2;
RESULT 753
ID  AAY69508 standard; protein; 562 AA.
DE  Acidothermus cellulolyticus E1 endoglucanase.
PN  CA2226898-A1.
PD  25-SEP-1999.
PA  (MIDE ) MIDWEST RES INST.
    Query Match      5.4%;  Score 118.5; DB 3;  Length 562;
    Best Local Similarity   24.1%;  Pred. No. 1.4;
RESULT 754
ID  AAU79549 standard; protein; 562 AA.
DE  A. cellulolyticus cellulase E1 beta-1,4-endoglucanse precursor.
PN  WO200234926-A2.
PD  02-MAY-2002.
PA  (UNMS ) UNIV MICHIGAN STATE.
    Query Match      5.4%;  Score 118.5; DB 5;  Length 562;
    Best Local Similarity   24.1%;  Pred. No. 1.4;
RESULT 755
ID  ADX96680 standard; protein; 929 AA.
DE  Plant full length insert polypeptide seqid 59344.
PN  US20040034888-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.
    Query Match      5.4%;  Score 118.5; DB 8;  Length 929;
    Best Local Similarity   24.8%;  Pred. No. 2.8;
RESULT 756
ID  ADH48699 standard; protein; 995 AA.
DE  Yeast hydrophobicity-related protein, SEQ ID NO:3.
PN  JP2003325179-A.
PD  18-NOV-2003.
PA  (TOYM ) TOYOBO KK.
PA  (KYOT-) KYOTO-SHI.
PA  (YAMA/) YAMAMOTO Y.
PA  (HIRO/) HIROOKA H.
    Query Match      5.4%;  Score 118.5; DB 8;  Length 995;
    Best Local Similarity   19.6%;  Pred. No. 3.1;
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RESULT 757
ID   AAU35339 standard; protein; 1031 AA.
DE   Enterococcus faecalis cellular proliferation protein #626.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.4%; Score 118.5; DB 4; Length 1031;
     Best Local Similarity   23.8%; Pred. No. 3.3;

RESULT 758
ID   ABU29451 standard; protein; 1061 AA.
DE   Protein encoded by Prokaryotic essential gene #14978.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.4%; Score 118.5; DB 6; Length 1061;
     Best Local Similarity   23.9%; Pred. No. 3.4;

RESULT 759
ID   ABB69720 standard; protein; 1126 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 35952.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.4%; Score 118.5; DB 4; Length 1126;
     Best Local Similarity   25.8%; Pred. No. 3.7;

RESULT 760
ID   ABP43711 standard; protein; 1497 AA.
DE   Bullous pemhigoid autoantigen BP180 gene.
PN   WO200231111-A2.
PD   18-APR-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.4%; Score 118.5; DB 5; Length 1497;
     Best Local Similarity   21.7%; Pred. No. 5.6;

RESULT 761
ID   ADA83846 standard; protein; 1497 AA.
DE   Human COL17A1 protein.
PN   WO200210328-A2.
PD   27-DEC-2002.
PA   (BIOM-) BIOMEDICAL CENT.
     Query Match   5.4%; Score 118.5; DB 6; Length 1497;
     Best Local Similarity   21.8%; Pred. No. 5.6;

RESULT 762
ID   AED74086 standard; protein; 1532 AA.
DE   Human placental protein SEQ ID NO:914.
PN   US200525114-A1.
PD   17-NOV-2005.
PA   (NUVE-) NUVELO INC.
     Query Match   5.4%; Score 118.5; DB 9; Length 1532;
     Best Local Similarity   21.8%; Pred. No. 5.8;

RESULT 763
ID   AAY83762 standard; protein; 371 AA.
DE   Encephalitozoon intestinalis polar tube protein PTP55.
PN   WO200001724-A1.
PD   13-JAN-2000.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   5.3%; Score 118; DB 3; Length 371;
     Best Local Similarity   26.3%; Pred. No. 0.85;

RESULT 764
ID   AAU96093 standard; protein; 496 AA.
DE   RhCMV unique short region US28.5 protein.
PN   WO200218954-A2.
PD   07-MAR-2002.
PA   (CHEM-) CHEMOCENTRYX INC.
     Query Match   5.3%; Score 118; DB 5; Length 496;
     Best Local Similarity   22.1%; Pred. No. 1.3;

RESULT 765
ID   AAW39927 standard; protein; 789 AA.
DE   Human Arnt receptor protein.
PN   DE19628894-A1.
PD   22-JAN-1998.
PA   (HAGE/)) HAGENMAIER H.
     Query Match   5.3%; Score 118; DB 2; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 766
ID   AAE24213 standard; protein; 789 AA.
DE   Human HIF-lbeta protein.
PN   WO200234291-A2.
PD   02-MAY-2002.
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
     Query Match   5.3%; Score 118; DB 5; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 767
ID   ABR82376 standard; protein; 789 AA.
DE   Hypoxia-inducible factor 1 (HIF-1) beta protein sequence.
PN   WO200305820-A2.
PD   17-JUL-2003.
PA   (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
     Query Match   5.3%; Score 118; DB 6; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 768
ID   ADE62808 standard; protein; 789 AA.
DE   Human Protein P27540, SEQ ID NO 8741.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.3%; Score 118; DB 7; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 769
ID   AEA81149 standard; protein; 789 AA.
DE   Human aryl hydrocarbon receptor nuclear translocator (ARNT) protein.
PN   US200513646 5-A1.
PD   23-JUN-2005.
PA   (CLER/) CLERC R G.
PA   (DUCH/) DUCHATEAU-NGUYEN G.
PA   (GARD/) GARDES C.
PA   (MIZR/) MIZRAHI J.
PA   (OSTE/) OSTENSON C.
     Query Match   5.3%; Score 118; DB 9; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 770
ID   AEF92066 standard; protein; 789 AA.
DE   Human aryl hydrocarbon nuclear receptor translocation (ARNT).
PN   WO200601982 4-A2.
PD   23-FEB-2006.
PA   (JOSL-) JOSLIN DIABETES CENT INC.
     Query Match   5.3%; Score 118; DB 10; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 771
ID   AEH64947 standard; protein; 789 AA.
DE   Human aryl hydrocarbon receptor nucleus translocator (Arnt1), SEQ ID 40.
PN   JP2005253434-A.
PD   22-SEP-2005.
PA   (HOKK-) HOKKAIDO TLO KK.
     Query Match   5.3%; Score 118; DB 10; Length 789;
     Best Local Similarity   24.2%; Pred. No. 2.5;

RESULT 772
ID   ADH71768 standard; protein; 904 AA.
DE   Human protein of the invention NOV28n SEQ ID NO:664.
PN   WO200310155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.3%; Score 118; DB 8; Length 904;
     Best Local Similarity   21.1%; Pred. No. 3;

RESULT 773
ID   AAP50073 standard; protein; 907 AA.
DE   Epstein-Barr virus (EBV) outer surface protein.
PN   EP151079-A.
PD   07-AUG-1985.
PA   (UYCH-) UNIV CHICAGO.
     Query Match   5.3%; Score 118; DB 1; Length 907;
     Best Local Similarity   23.4%; Pred. No. 3;

RESULT 774
ID   AAR80144 standard; protein; 907 AA.
DE   EBV gp350/220.
PN   WO9528488-A1.
PD   26-OCT-1995.

PA   (AVIR-) AVIRON.
      Query Match   5.3%;   Score 118; DB 2; Length 907;
      Best Local Similarity   23.4%;   Pred. No. 3;
RESULT 775
ID   AAY68009 standard; protein; 907 AA.
DE   Epstein-Barr virus major outer envelope glycoprotein Gp350.
PN   WO9964603-A2.
PD   16-DEC-1999.
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PA   (MOND/) MOND J J.
PA   (LEES/) LEES A.
      Query Match   5.3%;   Score 118; DB 3; Length 907;
      Best Local Similarity   23.4%;   Pred. No. 3;
RESULT 776
ID   AEB45568 standard; protein; 1130 AA.
DE   Alicyclobacillus sp. functional polypeptide, SEQ ID NO: 42.
PN   US2005147983-A1.
PD   07-JUL-2005.
PA   (NOVO) NOVOZYMES AS.
      Query Match   5.3%;   Score 118; DB 9; Length 1130;
      Best Local Similarity   20.2%;   Pred. No. 4.1;
RESULT 777
ID   AEB48754 standard; protein; 1130 AA.
DE   Alicyclobacillus sp. DSM 15716 functional polypeptide.
PN   WO2005066339-A2.
PD   21-JUL-2005.
PA   (NOVO) NOVOZYMES AS.
      Query Match   5.3%;   Score 118; DB 9; Length 1130;
      Best Local Similarity   20.2%;   Pred. No. 4.1;
RESULT 778
ID   ABB70311 standard; protein; 418 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 37725.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
      Query Match   5.3%;   Score 117.5; DB 4; Length 418;
      Best Local Similarity   26.9%;   Pred. No. 1.1;
RESULT 779
ID   ADA89591 standard; protein; 761 AA.
DE   Staphylococcus aureus antigenic protein #130.
PN   WO2003011899-A2.
PD   13-FEB-2003.
PA   (UYSH-) UNIV SHEFFIELD.
PA   (BIOS-) BIOSYNEXUS INC.
      Query Match   5.3%;   Score 117.5; DB 6; Length 761;
      Best Local Similarity   21.2%;   Pred. No. 2.6;
RESULT 780
ID   ABG70126 standard; protein; 1094 AA.
DE   Human prey protein for Shigella ipaD #3.
PN   WO200257303-A2.
PD   25-JUL-2002.
PA   (HYBR-) HYBRIGENICS.
      Query Match   5.3%;   Score 117.5; DB 5; Length 1094;
      Best Local Similarity   27.3%;   Pred. No. 4.3;
RESULT 781
ID   AEL55889 standard; protein; 1262 AA.
DE   Mouse MKIAA1930 protein, SEQ ID NO. 350.
PN   US2006216722-A1.
PD   28-SEP-2006.
PA   (BETS/) BETSHOLTZ C.
PA   (TRYG/) TRYGGVASON K.
PA   (TAKE/) TAKEMOTO M.
PA   (HELL/) HE L.
PA   (PATR/) PATRAKKAS J.
      Query Match   5.3%;   Score 117.5; DB 10; Length 1262;
      Best Local Similarity   20.9%;   Pred. No. 5.3;
RESULT 782
ID   ADJ70186 standard; protein; 1417 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqId1992.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.

      Query Match   5.3%;   Score 117.5; DB 7; Length 1417;
      Best Local Similarity   21.8%;   Pred. No. 6.2;
RESULT 783
ID   ABR58656 standard; protein; 1482 AA.
DE   Human cancer related protein SEQ ID NO.313.
PN   WO200305138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
      Query Match   5.3%;   Score 117.5; DB 6; Length 1482;
      Best Local Similarity   24.2%;   Pred. No. 6.6;
RESULT 784
ID   ADU91598 standard; protein; 1541 AA.
DE   Yeast raptor protein.
PN   WO200402276-A2.
PD   08-APR-2004.
PA   (WHED) WHITEHEAD INST BIOMEDICAL RES.
      Query Match   5.3%;   Score 117.5; DB 8; Length 1541;
      Best Local Similarity   21.4%;   Pred. No. 7;
RESULT 785
ID   ADO30907 standard; protein; 2089 AA.
DE   Human Polo-like kinase-related protein MDC1 domain SeqID28.
PN   WO200404317-A2.
PD   03-JUN-2004.
PA   (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA   (YAFF/) YAFFE M B.
PA   (ELIA/) ELIA A E H.
PA   (RELL/) RELLOS P.
PA   (CANT/) CANTLEY L C.
PA   (SMER/) SMERDON S J.
PA   (MANC/) MANCKE I.
      Query Match   5.3%;   Score 117.5; DB 8; Length 2089;
      Best Local Similarity   21.3%;   Pred. No. 11;
RESULT 786
ID   AEJ97331 standard; protein; 2089 AA.
DE   Human apoptosis inhibitor with p53 binding activity, SEQ ID 13.
PN   JP200622265-A.
PD   31-AUG-2006.
PA   (HISM) HISAMITSU PHARM CO LTD.
PA   (CHIB-) CHIBA PREFECTURE.
      Query Match   5.3%;   Score 117.5; DB 10; Length 2089;
      Best Local Similarity   21.3%;   Pred. No. 11;
RESULT 787
ID   ABG21256 standard; protein; 2114 AA.
DE   Novel human diagnostic protein #21247.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
      Query Match   5.3%;   Score 117.5; DB 4; Length 2114;
      Best Local Similarity   22.9%;   Pred. No. 11;
RESULT 788
ID   ABO00861 standard; protein; 2114 AA.
DE   Polypeptide encoded by novel human contig #112.
PN   WO2003023013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.
      Query Match   5.3%;   Score 117.5; DB 6; Length 2114;
      Best Local Similarity   22.9%;   Pred. No. 11;
RESULT 789
ID   AEH63700 standard; protein; 3838 AA.
DE   Enterobacter cloacae protein amino acid sequence - SEQ ID 10137.
PN   US7041814-B1.
PD   09-MAY-2006.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match   5.3%;   Score 117.5; DB 10; Length 3838;
      Best Local Similarity   23.1%;   Pred. No. 26;
RESULT 790
ID   ABP07042 standard; protein; 128 AA.
DE   Human ORFX protein sequence SEQ ID NO.14066.
PN   WO200192523-A2.
PD   06-DEC-2001.
PA   (CURA-) CURAGEN CORP.
      Query Match   5.3%;   Score 117; DB 5; Length 128;
      Best Local Similarity   31.2%;   Pred. No. 0.23;

RESULT 791
ID AEA36681 standard; protein; 420 AA.
DE Equine P-selection glycoprotein ligand-1 (ePSGL-1) protein - SEQ ID 2.
PN WO200504732O-A2.)
PD 26-MAY-2005.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
PA (DARI/) DARIEN B J.
    Query Match   5.3%; Score 117; DB 9; Length 420;
    Best Local Similarity 23.4%; Pred. No. 1.2;

RESULT 792
ID ABG93105 standard; protein; 551 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 168.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
    Query Match   5.3%; Score 117; DB 5; Length 551;
    Best Local Similarity 21.8%; Pred. No. 1.8;

RESULT 793
ID AEH16836 standard; protein; 560 AA.
DE Candida albicans cell wall protein Rbr3p.
PN WO2005090397-A1.
PD 29-SEP-2005.
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN EV.
    Query Match   5.3%; Score 117; DB 10; Length 560;
    Best Local Similarity 24.0%; Pred. No. 1.8;

RESULT 794
ID AAB52440 standard; protein; 567 AA.
DE Mycobacterium tuberculosis secreted protein #5.
PN WO200066143-A1.
PD 09-NOV-2000.
PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
    Query Match   5.3%; Score 117; DB 4; Length 567;
    Best Local Similarity 23.6%; Pred. No. 1.9;

RESULT 795
ID ABB60943 standard; protein; 1412 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9621.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.3%; Score 117; DB 4; Length 1412;
    Best Local Similarity 21.8%; Pred. No. 6.8;

RESULT 796
ID ABP69627 standard; protein; 1497 AA.
DE Human polypeptide SEQ ID NO 1674.
PN WO20270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
    Query Match   5.3%; Score 117; DB 5; Length 1497;
    Best Local Similarity 24.1%; Pred. No. 7.4;

RESULT 797
ID ABB60186 standard; protein; 1714 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7350.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.3%; Score 117; DB 4; Length 1714;
    Best Local Similarity 23.9%; Pred. No. 9;

RESULT 798
ID ABB63911 standard; protein; 2016 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18525.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.3%; Score 117; DB 4; Length 2016;
    Best Local Similarity 24.7%; Pred. No. 11;

RESULT 799
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.3%; Score 116.5; DB 4; Length 183;
    Best Local Similarity 25.7%; Pred. No. 0.41;

RESULT 800
ID AAR07671 standard; protein; 278 AA.
DE Intestinal mucin deduced from clone SMUC 41.
PN WO9012892-A.
PD 01-NOV-1990.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.3%; Score 116.5; DB 2; Length 278;
    Best Local Similarity 26.9%; Pred. No. 0.75;

RESULT 801
ID AAR12535 standard; protein; 278 AA.
DE SMUC-41 intestinal mucin.
PN WO9108217-A.
PD 13-JUN-1991.
PA (REGC) UNIV CALIFORNIA.
    Query Match   5.3%; Score 116.5; DB 2; Length 278;
    Best Local Similarity 26.9%; Pred. No. 0.75;

RESULT 802
ID AAU15851 standard; protein; 450 AA.
DE Human novel secreted protein, Seq ID 804.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
    Query Match   5.3%; Score 116.5; DB 4; Length 450;
    Best Local Similarity 22.6%; Pred. No. 1.5;

RESULT 803
ID ABU54920 standard; protein; 450 AA.
DE Human novel polypeptide #7.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
    Query Match   5.3%; Score 116.5; DB 6; Length 450;
    Best Local Similarity 22.6%; Pred. No. 1.5;

RESULT 804
ID ABP73767 standard; protein; 515 AA.
DE Candida albicans essential protein SEQ ID NO 7604.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   5.3%; Score 116.5; DB 5; Length 515;
    Best Local Similarity 19.0%; Pred. No. 1.8;

RESULT 805
ID ADX74116 standard; protein; 551 AA.
DE Plant full length insert polypeptide seqid 43482.
PN US200403488-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
    Query Match   5.3%; Score 116.5; DB 8; Length 551;
    Best Local Similarity 24.9%; Pred. No. 2;

RESULT 806
ID ABM85536 standard; protein; 691 AA.
DE Mouse protein sequence mCP5967.
PN WO203073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
    Query Match   5.3%; Score 116.5; DB 7; Length 691;
    Best Local Similarity 22.1%; Pred. No. 2.7;

RESULT 807
ID ADT56299 standard; protein; 760 AA.
DE Plant polypeptide, SEQ ID 6376.
PN US200421619O-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
    Query Match   5.3%; Score 116.5; DB 8; Length 760;
    Best Local Similarity 19.6%; Pred. No. 3.1;

RESULT 808
ID ADZ03672 standard; protein; 1038 AA.

DE   PRG4-lub:3 protein.
PN   WO2005016130-A2.
PD   24-FEB-2005.
PA   (AMPH) WYETH.
     Query Match   5.3%; Score 116.5; DB 9; Length 1038
     Best Local Similarity   22.3%; Pred. No. 4.8;
RESULT 809
ID   ABB57802 standard; protein; 1164 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 198.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.3%; Score 116.5; DB 4; Length 1164;
     Best Local Similarity   20.5%; Pred. No. 5.7;
RESULT 810
ID   ADY07303 standard; protein; 1272 AA.
DE   Plant full length insert polypeptide seqid 63118.
PN   US20040348881-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   5.3%; Score 116.5; DB 8; Length 1272;
     Best Local Similarity   21.2%; Pred. No. 6.5;
RESULT 811
ID   ABB60228 standard; protein; 1624 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 7476.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.3%; Score 116.5; DB 4; Length 1624;
     Best Local Similarity   23.6%; Pred. No. 9.1;
RESULT 812
ID   AAU34408 standard; protein; 502 AA.
DE   Staphylococcus aureus cellular proliferation protein #684.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.2%; Score 116; DB 4; Length 502;
     Best Local Similarity   24.6%; Pred. No. 1.9;
RESULT 813
ID   ADV99546 standard; protein; 510 AA.
DE   Human soluble stimulator of endothelial proliferation, sSEP #12.
PN   WO2004111085-A1.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
     Query Match   5.2%; Score 116; DB 9; Length 510;
     Best Local Similarity   21.6%; Pred. No. 1.9;
RESULT 814
ID   ADW43180 standard; protein; 510 AA.
DE   Human soluble SEP' (sSEP) protein fragment - SEQ ID 18.
PN   WO2004111085-A1.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
     Query Match   5.2%; Score 116; DB 9; Length 510;
     Best Local Similarity   21.6%; Pred. No. 1.9;
RESULT 815
ID   ADV99532 standard; protein; 540 AA.
DE   Human membrane -bound stimulator of endothelial proliferation, SEP #1.
PN   WO2004111085-A1.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
     Query Match   5.2%; Score 116; DB 9; Length 540;
     Best Local Similarity   21.6%; Pred. No. 2.1;
RESULT 816
ID   ADW43166 standard; protein; 540 AA.
DE   Human membrane-bound angiogenic factor SEP protein - SEQ ID 4.
PN   WO2004111088-A2.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.

     Query Match   5.2%; Score 116; DB 9; Length 540;
     Best Local Similarity   21.6%; Pred. No. 2.1;
RESULT 817
ID   AAU37464 standard; protein; 560 AA.
DE   Staphylococcus aureus cellular proliferation protein #1634.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.2%; Score 116; DB 4; Length 560;
     Best Local Similarity   24.6%; Pred. No. 2.2;
RESULT 818
ID   ABU04080 standard; protein; 603 AA.
DE   Protein encoded by Prokaryotic essential gene #29607.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.2%; Score 116; DB 6; Length 603;
     Best Local Similarity   21.9%; Pred. No. 2.5;
RESULT 819
ID   ABB57801 standard; protein; 730 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 195.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.2%; Score 116; DB 4; Length 730;
     Best Local Similarity   22.2%; Pred. No. 3.2;
RESULT 820
ID   AEB53801 standard; protein; 906 AA.
DE   Drosophila nuclear receptor #15.
PN   WO200506959-A2.
PD   04-AUG-2005.
PA   (UTAH) UNIV UTAH RES FOUND.
     Query Match   5.2%; Score 116; DB 9; Length 906;
     Best Local Similarity   22.3%; Pred. No. 4.4;
RESULT 821
ID   AAW00634 standard; protein; 985 AA.
DE   ILTV glycoprotein g60.
PN   WO9508622-A1.
PD   30-MAR-1995.
PA   (SYTR) SYNTRO CORP.
     Query Match   5.2%; Score 116; DB 2; Length 985;
     Best Local Similarity   21.8%; Pred. No. 4.9;
RESULT 822
ID   AAW06786 standard; protein; 985 AA.
DE   ILTV glycoprotein g60.
PN   WO9629396-A1.
PD   26-SEP-1996.
PA   (SYTR) SYNTRO CORP.
     Query Match   5.2%; Score 116; DB 2; Length 985;
     Best Local Similarity   21.8%; Pred. No. 4.9;
RESULT 823
ID   ABG03621 standard; protein; 1022 AA.
DE   Novel human diagnostic protein #3612.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.2%; Score 116; DB 4; Length 1022;
     Best Local Similarity   20.8%; Pred. No. 5.2;
RESULT 824
ID   ABG08173 standard; protein; 1022 AA.
DE   Novel human diagnostic protein #8164.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.2%; Score 116; DB 4; Length 1022;
     Best Local Similarity   20.8%; Pred. No. 5.2;
RESULT 825
ID   ABG05826 standard; protein; 1022 AA.
DE   Novel human diagnostic protein #5817.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.2%; Score 116; DB 4; Length 1022;

Best Local Similarity 20.8%; Pred. No. 5.2:
RESULT 826
ID   ADD46005 standard; protein; 1199 AA.
DE   Rat Protein P52591, SEQ ID NO 11677.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.2%;   Score 116; DB 7; Length 1199;
     Best Local Similarity 21.7%; Pred. No. 6.5;
RESULT 827
ID   ADE61171 standard; protein; 1199 AA.
DE   Rat Protein P52591, SEQ ID NO 7089.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.2%;   Score 116; DB 7; Length 1199;
     Best Local Similarity 21.7%; Pred. No. 6.5;
RESULT 828
ID   AAR13791 standard; protein; 1237 AA.
DE   E75A protein.
PN   WO9113167-A.
PD   05-SEP-1991.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.2%;   Score 116; DB 2; Length 1237;
     Best Local Similarity 22.3%; Pred. No. 6.8;
RESULT 829
ID   AAE30117 standard; protein; 1237 AA.
DE   Fruit fly ecdysone-inducible protein 75A (E75A).
PN   WO200277157-A2.
PD   03-OCT-2002.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
     Query Match   5.2%;   Score 116; DB 3; Length 1237;
     Best Local Similarity 22.3%; Pred. No. 6.8;
RESULT 830
ID   AAB07974 standard; protein; 1247 AA.
DE   A murine neural plakophilin related armadillo protein.
PN   WO200047615-A2.
PD   17-AUG-2000.
PA   (UTOR) UNIV TORONTO GOVERNING COUNCIL.
     Query Match   5.2%;   Score 116; DB 3; Length 1247;
     Best Local Similarity 21.5%; Pred. No. 6.9;
RESULT 831
ID   ABB63705 standard; protein; 2065 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 17907.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.2%;   Score 116; DB 4; Length 2065;
     Best Local Similarity 22.3%; Pred. No. 14;
RESULT 832
ID   ADJ70512 standard; protein; 2090 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID2318.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   5.2%;   Score 116; DB 7; Length 2090;
     Best Local Similarity 21.1%; Pred. No. 14;
RESULT 833
ID   AAB11739 standard; protein; 130 AA.
DE   C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:13.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.2%;   Score 115.5; DB 3; Length 130;
     Best Local Similarity 26.4%; Pred. No. 0.31;
RESULT 834
ID   ABJ04052 standard; protein; 130 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 13.
PN   WO200194631-A1.
PD   13-DEC-2001.

PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.2%;   Score 115.5; DB 5; Length 130;
     Best Local Similarity 26.4%; Pred. No. 0.31;
RESULT 835
ID   AAG81183 standard; protein; 299 AA.
DE   Mycobacterium tuberculosis potential drug target protein SEQ ID 234.
PN   WO200135317-A1.
PD   17-MAY-2001.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.2%;   Score 115.5; DB 4; Length 299;
     Best Local Similarity 22.6%; Pred. No. 1;
RESULT 836
ID   ABU36744 standard; protein; 299 AA.
DE   Protein encoded by Prokaryotic essential gene #22271.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.2%;   Score 115.5; DB 6; Length 299;
     Best Local Similarity 22.6%; Pred. No. 1;
RESULT 837
ID   ABU34423 standard; protein; 299 AA.
DE   Protein encoded by Prokaryotic essential gene #19950.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.2%;   Score 115.5; DB 6; Length 299;
     Best Local Similarity 22.6%; Pred. No. 1;
RESULT 838
ID   AAW35855 standard; protein; 319 AA.
DE   Human CD43 for use in T lymphocyte veto molecule.
PN   WO9737687-A1.
PD   16-OCT-1997.
PA   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
     Query Match   5.2%;   Score 115.5; DB 2; Length 319;
     Best Local Similarity 26.2%; Pred. No. 1.1;
RESULT 839
ID   ADZ51063 standard; protein; 778 AA.
DE   Amino acid sequence of murine CD44.
PN   WO2005034984-A1.
PD   21-APR-2005.
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
     Query Match   5.2%;   Score 115.5; DB 9; Length 778;
     Best Local Similarity 25.2%; Pred. No. 3.9;
RESULT 840
ID   ADU02303 standard; protein; 264 AA.
DE   Novel human polypeptide seqid 770.
PN   WO2004093804-A2.
PD   04-NOV-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
     Query Match   5.2%;   Score 115; DB 8; Length 264;
     Best Local Similarity 20.5%; Pred. No. 0.92;
RESULT 841
ID   ADI17288 standard; protein; 359 AA.
DE   Polypeptide homologous to a human NOVX domain SeqID 824.
PN   WO2003002722-A2.
PD   06-SEP-2002.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.2%;   Score 115; DB 5; Length 359;
     Best Local Similarity 23.4%; Pred. No. 1.4;
RESULT 842
ID   ABP70447 standard; protein; 378 AA.
DE   Amino acid sequence of human TIM-4 allele 2.
PN   WO2003002722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.2%;   Score 115; DB 6; Length 378;
     Best Local Similarity 26.0%; Pred. No. 1.5;
RESULT 843
ID   ADY98089 standard; protein; 378 AA.
DE   Human TIM-4 allele 2-encoded protein.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.

PA   (DAND) DANA FARBER CANCER INST INC.
Query Match   5.2%; Score 115; DB 9; Length 378;
Best Local Similarity 26.0%; Pred. No. 1.5;
RESULT 844
ID   AED60533 standard; protein; 378 AA.
DE   Human TIM-4, allele 1, protein SEQ ID NO:41.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
Query Match   5.2%; Score 115; DB 9; Length 378;
Best Local Similarity 26.0%; Pred. No. 1.5;
RESULT 845
ID   ABB82899 standard; protein; 400 AA.
DE   Human CD43 protein.
PN   WO2002101071-A2.
PD   19-DEC-2002.
PA   (RIGE-) RIGEL PHARM INC.
Query Match   5.2%; Score 115; DB 6; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 846
ID   ADD25564 standard; protein; 400 AA.
DE   Binding domain-immunoglobulin fusion protein-associated protein #59.
PN   US2003118592-A1.
PD   26-JUN-2003.
PA   (GENE-) GENECRAFT INC.
Query Match   5.2%; Score 115; DB 7; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 847
ID   ABM85587 standard; protein; 400 AA.
DE   Human protein sequence hCP1690086.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
Query Match   5.2%; Score 115; DB 7; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 848
ID   ADM41103 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:4.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 849
ID   ADM41109 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:10.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 850
ID   ADM41101 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:2.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 851
ID   ADM41113 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:14.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 852
ID   ADM41105 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:6.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.

Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 853
ID   ADM41111 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:12.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 854
ID   ADM41107 standard; protein; 400 AA.
DE   Human CD43 (sialophorin, leukosialin) protein, SEQ ID NO:8.
PN   WO2004026120-A2.
PD   01-APR-2004.
PA   (GEHO) GEN HOSPITAL CORP.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 855
ID   ABO58519 standard; protein; 400 AA.
DE   Human genome derived single exon protein #4753.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 856
ID   ABM81750 standard; protein; 400 AA.
DE   Tumour-associated antigenic target (TAT) polypeptide PRO2355, SEQ:4512.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   5.2%; Score 115; DB 8; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 857
ID   ADZ13125 standard; protein; 400 AA.
DE   Human cancer-associated protein #199.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR) CHIRON CORP.
Query Match   5.2%; Score 115; DB 9; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 858
ID   ADZ13127 standard; protein; 400 AA.
DE   Human cancer-associated protein #200.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR) CHIRON CORP.
Query Match   5.2%; Score 115; DB 9; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 859
ID   AEC31160 standard; protein; 400 AA.
DE   Human CD43 SEQ ID NO 1.
PN   WO2005081904-A2.
PD   09-SEP-2005.
PA   (BURN-) BURNHAM INST.
PA   (UYSH-) UNIV SHINSHU.
Query Match   5.2%; Score 115; DB 9; Length 400;
Best Local Similarity 26.1%; Pred. No. 1.7;
RESULT 860
ID   AED49058 standard; protein; 505 AA.
DE   Dust mite allergen #2.
PN   WO2005097996-A1.
PD   20-OCT-2005.
PA   (NIZE-) NIPPON ZENYAKU KOGYO LTD.
Query Match   5.2%; Score 115; DB 9; Length 505;
Best Local Similarity 24.1%; Pred. No. 2.3;
RESULT 861
ID   ADV99535 standard; protein; 508 AA.
DE   Human soluble stimulator of endothelial proliferation, sSEP #1.
PN   WO2004111085-A1.

PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
     Query Match   5.2%; Score 115; DB 9; Pred. No. 2.3;
     Best Local Similarity 21.6%;
     Length 508;
RESULT 862
ID   ADW43169 standard; protein; 508 AA.
DE   Human soluble SEP (sSEP) protein fragment - SEQ ID 7.
PN   WO2004011088-A2.
PD   23-DEC-2004.
PA   (XANT-) XANTOS BIOMEDICINE AG.
     Query Match   5.2%; Score 115; DB 9; Pred. No. 2.3;
     Best Local Similarity 21.6%;
     Length 508;
RESULT 863
ID   AAY52525 standard; protein; 536 AA.
DE   House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
PN   WO9954349-A2.
PD   28-OCT-1999.
PA   (HESK-) HESKA CORP.
     Query Match   5.2%; Score 115; DB 3; Pred. No. 2.5;
     Best Local Similarity 21.8%;
     Length 536;
RESULT 864
ID   AAU96329 standard; protein; 536 AA.
DE   Der HMW-map polypeptide #16.
PN   WO20022807-A2.
PD   21-MAR-2002.
PA   (HESK-) HESKA CORP.
     Query Match   5.2%; Score 115; DB 5; Pred. No. 2.5;
     Best Local Similarity 21.8%;
     Length 536;
RESULT 865
ID   AAY52523 standard; protein; 555 AA.
DE   House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
PN   WO9954349-A2.
PD   28-OCT-1999.
PA   (HESK-) HESKA CORP.
     Query Match   5.2%; Score 115; DB 3; Pred. No. 2.6;
     Best Local Similarity 21.8%;
     Length 555;
RESULT 866
ID   AAU96327 standard; protein; 555 AA.
DE   Der HMW-map polypeptide #14.
PN   WO20022807-A2.
PD   21-MAR-2002.
PA   (HESK-) HESKA CORP.
     Query Match   5.2%; Score 115; DB 5; Pred. No. 2.6;
     Best Local Similarity 21.8%;
     Length 555;
RESULT 867
ID   AAU96328 standard; protein; 555 AA.
DE   Der HMW-map polypeptide #15.
PN   WO20022807-A2.
PD   21-MAR-2002.
PA   (HESK-) HESKA CORP.
     Query Match   5.2%; Score 115; DB 5; Pred. No. 2.6;
     Best Local Similarity 21.8%;
     Length 555;
RESULT 868
ID   ABU50302 standard; protein; 921 AA.
DE   Protein encoded by Prokaryotic essential gene #35829.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.2%; Score 115; DB 6; Pred. No. 5.4;
     Best Local Similarity 35.1%;
     Length 921;
RESULT 869
ID   AD203664 standard; protein; 981 AA.
DE   PRG4-Lub:1 protein.
PN   WO2005016130-A2.
PD   24-FEB-2005.
PA   (AMHP) WYETH.
     Query Match   5.2%; Score 115; DB 9; Pred. No. 5.9;
     Best Local Similarity 22.9%;
     Length 981;
RESULT 870
ID   ABU09232 standard; protein; 1167 AA.
DE   Rat neuropathic pain gene 4, NPG4, polypeptide.
PN   US2003003538-A1.
PD   02-JAN-2003.

PA   (DIET/) DIETRICH P S.
PA   (HUAN/) HUANG C.
PA   (JOHN/) JOHNSON C D.
PA   (SANG/) SANGAMESWARAN L.
     Query Match   5.2%; Score 115; DB 6; Pred. No. 7.6;
     Best Local Similarity 20.6%;
     Length 1167;
RESULT 871
ID   ADR18912 standard; protein; 1994 AA.
DE   Human mucin-like protein, SCS0004, SEQ ID 2.
PN   WO2004069136-A2.
PD   19-AUG-2004.
PA   (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
     Query Match   5.2%; Score 115; DB 8; Pred. No. 16;
     Best Local Similarity 24.7%;
     Length 1994;
RESULT 872
ID   AAB53193 standard; protein; 2548 AA.
DE   Macaca mulatta rhadinovirus 17577 RRV ORF64 protein SEQ ID NO:143.
PN   WO200028040-A2.
PD   18-MAY-2000.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match   5.2%; Score 115; DB 3; Pred. No. 23;
     Best Local Similarity 24.6%;
     Length 2548;
RESULT 873
ID   AAB11740 standard; protein; 130 AA.
DE   C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:14.
PN   US6071518-A.
PD   06-JUN-2000.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.2%; Score 114.5; DB 3; Pred. No. 0.37;
     Best Local Similarity 27.2%;
     Length 130;
RESULT 874
ID   ABJ04053 standard; protein; 130 AA.
DE   C parvum GP900 protein fragment SEQ ID NO: 14.
PN   WO200194631-A1.
PD   13-DEC-2001.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   5.2%; Score 114.5; DB 5; Pred. No. 0.37;
     Best Local Similarity 27.2%;
     Length 130;
RESULT 875
ID   ABG91405 standard; protein; 468 AA.
DE   Primate LP282.
PN   WO200263009-A2.
PD   15-AUG-2002.
PA   (ELIL) LILLY & CO ELI.
     Query Match   5.2%; Score 114.5; DB 5; Pred. No. 2.3;
     Best Local Similarity 21.2%;
     Length 468;
RESULT 876
ID   ABR43261 standard; protein; 468 AA.
DE   Human PMM-22 protein SEQ ID NO:22.
PN   WO2003025131-A2.
PD   27-MAR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   5.2%; Score 114.5; DB 6; Pred. No. 2.3;
     Best Local Similarity 21.2%;
     Length 468;
RESULT 877
ID   AAM14883 standard; protein; 511 AA.
DE   Peptide #1317 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.2%; Score 114.5; DB 4; Pred. No. 2.6;
     Best Local Similarity 23.8%;
     Length 511;
RESULT 878
ID   ABB33852 standard; peptide; 511 AA.
DE   Peptide #1358 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.2%; Score 114.5; DB 4; Pred. No. 2.6;
     Best Local Similarity 23.8%;
     Length 511;
RESULT 879
ID   AAM27312 standard; protein; 511 AA.
DE   Peptide #1349 encoded by probe for measuring placental gene expression.

PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 880
ID   ABB28667 standard; peptide; 511 AA.
DE   Peptide #1318 encoded by breast cell single exon nucleic acid probe.
PN   WO200157271-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 881
ID   ABB19292 standard; protein; 511 AA.
DE   Protein #1291 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 882
ID   AAM67022 standard; protein; 511 AA.
DE   Human bone marrow expressed single exon probe encoded protein SEQ ID NO: 27328.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 883
ID   AAM54616 standard; protein; 511 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 26721.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 884
ID   ABG48687 standard; peptide; 511 AA.
DE   Human liver peptide, SEQ ID No 27335.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 885
ID   AAM02607 standard; protein; 511 AA.
DE   Peptide #1289 encoded by probe for measuring breast gene expression.
PN   WO200157270-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 5; Length 511;
      Best Local Similarity   23.8%;   Pred. No. 2.6;
RESULT 886
ID   ABG36679 standard; peptide; 511 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 26344.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
      Query Match   5.2%;   Score 114.5; DB 4; Length 514;
      Best Local Similarity   23.0%;   Pred. No. 2.6;
RESULT 887
ID   AAB92523 standard; protein; 514 AA.
DE   Human protein sequence SEQ ID NO:10672.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
      Query Match   5.2%;   Score 114.5; DB 4; Length 545;
      Best Local Similarity   23.0%;   Pred. No. 2.6;
RESULT 888
ID   ABO58646 standard; protein; 545 AA.
DE   Human genome derived single exon protein #4880.
PN   US2003194704-A1.

PN   WO200157272-A2.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
      Query Match   5.2%;   Score 114.5; DB 8; Length 545;
      Best Local Similarity   23.8%;   Pred. No. 2.8;
RESULT 889
ID   ADM12422 standard; protein; 660 AA.
DE   Human melanocyte protein gp 100/Pmel 17.
PN   US200323594-A1.
PD   25-DEC-2003.
PA   (ANTI-) ANTIGEN EXPRESS INC.
      Query Match   5.2%;   Score 114.5; DB 8; Length 660;
      Best Local Similarity   21.9%;   Pred. No. 3.7;
RESULT 890
ID   ADO38644 standard; protein; 660 AA.
DE   Melanocyte protein Pmel/gp100.
PN   US200405881-A1.
PD   25-MAR-2004.
PA   (ANTI-) ANTIGEN EXPRESS INC.
      Query Match   5.2%;   Score 114.5; DB 8; Length 660;
      Best Local Similarity   21.9%;   Pred. No. 3.7;
RESULT 891
ID   AEF01130 standard; protein; 660 AA.
DE   Melanocyte protein gp100/ Pmel 17, SEQ ID 385.
PN   US200600294/-Al.
PD   05-JAN-2006.
PA   (HUMP/) HUMPHREYS R.
PA   (XUMM/) XU M.
      Query Match   5.2%;   Score 114.5; DB 10; Length 660;
      Best Local Similarity   21.9%;   Pred. No. 3.7;
RESULT 892
ID   ABU05689 standard; protein; 293 AA.
DE   M. tuberculosis and M. leprae marker protein #340.
PN   WO20027490-A2.
PD   26-SEP-2002.
PA   (INSP) INST PASTEUR.
      Query Match   5.2%;   Score 114; DB 5; Length 293;
      Best Local Similarity   21.4%;   Pred. No. 1.3;
RESULT 893
ID   ADE63885 standard; protein; 442 AA.
DE   Rat Protein CAA44848, SEQ ID NO 9831.
PN   WO200301647-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
      Query Match   5.2%;   Score 114; DB 7; Length 442;
      Best Local Similarity   23.1%;   Pred. No. 2.3;
RESULT 894
ID   ADS43560 standard; protein; 507 AA.
DE   Bacterial polypeptide #21990.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
      Query Match   5.2%;   Score 114; DB 8; Length 507;
      Best Local Similarity   21.6%;   Pred. No. 2.8;
RESULT 895
ID   AAO13658 standard; protein; 530 AA.
DE   Human polypeptide SEQ ID NO 27550.
PN   WO200164835-A2.
PD   07-SEP-2001.
PA   (HYSB-) HYSEQ INC.
      Query Match   5.2%;   Score 114; DB 4; Length 530;
      Best Local Similarity   23.8%;   Pred. No. 3;
RESULT 896
ID   AAW0762 standard; protein; 540 AA.
DE   Interleukin binding factor ILF-1.
PN   US553631-A.
PD   09-JUL-1996.

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PA  (TEXA ) UNIV TEXAS SYSTEM.
    Query Match           5.2%;    Score 114; DB 2; Length 540;
    Best Local Similarity  23.2%;  Pred. No. 3.1;
RESULT 897
ID  ADN72473 standard; protein; 580 AA.
DE  Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 368.
PN  WO2004035798-A2.
PD  29-APR-2004.
PA  (CROP-) CROPDESIGN NV.
    Query Match           5.2%;    Score 114; DB 8; Length 580;
    Best Local Similarity  24.6%;  Pred. No. 3.4;
RESULT 898
ID  ADI82525 standard; protein; 655 AA.
DE  Human modifier of p21 (MP21) protein sequence SeqID91.
PN  WO2004005486-A2.
PD  15-JAN-2004.
PA  (EXEL-) EXELIXIS INC.
    Query Match           5.2%;    Score 114; DB 8; Length 655;
    Best Local Similarity  23.2%;  Pred. No. 4;
RESULT 899
ID  ADX07713 standard; protein; 655 AA.
DE  Cyclin-dependent kinase modulation biomarker SEQ ID NO 2278.
PN  WO2005012875-A2.
PD  10-FEB-2005.
PA  (BRIM-) BRISTOL-MYERS SQUIBB CO.
    Query Match           5.2%;    Score 114; DB 9; Length 655;
    Best Local Similarity  23.2%;  Pred. No. 4;
RESULT 900
ID  ADI42548 standard; protein; 682 AA.
DE  Plant transcription factor #366.
PN  US2004019927-A1.
PD  29-JAN-2004.
PA  (SHER/) SHERMAN B K.
PA  (RIEC/) RIECHMANN J L.
PA  (JIAN/) JIANG C.
PA  (HEAR/) HEARD J E.
PA  (HAAK/) HAAKE V.
PA  (CREE/) CREELMAN R A.
PA  (RATC/) RATCLIFFE O.
PA  (ADAM/) ADAM L J.
PA  (REUB/) REUBER T L.
PA  (KEDD/) KEDDIE J.
PA  (BROU/) BROUN P E.
PA  (PILG/) PILGRIM M L.
PA  (DUBE/) DUBELL A N.
PA  (PINE/) PINEDA O.
PA  (YUGG/) YU G.
    Query Match           5.2%;    Score 114; DB 8; Length 682;
    Best Local Similarity  22.8%;  Pred. No. 4.3;
RESULT 901
ID  ABB58267 standard; protein; 1013 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 1593.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match           5.2%;    Score 114; DB 4; Length 1013;
    Best Local Similarity  25.1%;  Pred. No. 7.5;
RESULT 902
ID  ADV97875 standard; protein; 2132 AA.
DE  Murine protein kinase enzyme Seq 195.
PN  WO2005000200-A2.
PD  06-JAN-2005.
PA  (SUGE-) SUGEN INC.
    Query Match           5.2%;    Score 114; DB 9; Length 2132;
    Best Local Similarity  30.2%;  Pred. No. 22;
RESULT 903
ID  AAY57453 standard; protein; 2781 AA.
DE  Human transcriptional regulatory factor SEQ ID NO:10.
PN  WO9957143-A1.
PD  11-NOV-1999.
PA  (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
    Query Match           5.2%;    Score 114; DB 3; Length 2781;
    Best Local Similarity  21.5%;  Pred. No. 31;

RESULT 904
ID  ADF42724 standard; protein; 2781 AA.
DE  Human BPFF amino acid sequence SEQ ID NO.30.
PN  WO2003102163-A2.
PD  11-DEC-2003.
PA  (META-) METABOLEX INC.
    Query Match           5.2%;    Score 114; DB 8; Length 2781;
    Best Local Similarity  21.5%;  Pred. No. 31;
RESULT 905
ID  ADO00984 standard; protein; 2781 AA.
DE  Human homologue of Fruit fly AD-related protein CG17135.
PN  US2004067535-A1.
PD  08-APR-2004.
PA  (LIFE-) LIFE SCI DEV CORP.
    Query Match           5.2%;    Score 114; DB 8; Length 2781;
    Best Local Similarity  21.5%;  Pred. No. 31;
RESULT 906
ID  ADQ18653 standard; protein; 2781 AA.
DE  Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.
PN  WO2004048938-A2.
PD  10-JUN-2004.
PA  (PROT-) PROTEIN DESIGN LABS INC.
    Query Match           5.2%;    Score 114; DB 8; Length 2781;
    Best Local Similarity  21.5%;  Pred. No. 31;
RESULT 907
ID  AAY57452 standard; protein; 2907 AA.
DE  Human transcriptional regulatory factor SEQ ID NO:1.
PN  WO9957143-A1.
PD  11-NOV-1999.
PA  (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
    Query Match           5.2%;    Score 114; DB 3; Length 2907;
    Best Local Similarity  21.5%;  Pred. No. 33;
RESULT 908
ID  AAB11738 standard; protein; 128 AA.
DE  C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:12.
PN  US6071518-A.
PD  06-JUN-2000.
PA  (REGC ) UNIV CALIFORNIA.
    Query Match           5.1%;    Score 113.5; DB 3; Length 128;
    Best Local Similarity  26.4%;  Pred. No. 0.44;
RESULT 909
ID  ABJ04051 standard; protein; 128 AA.
DE  C parvum GP900 protein fragment SEQ ID NO: 12.
PN  WO200194631-A1.
PD  13-DEC-2001.
PA  (REGC ) UNIV CALIFORNIA.
    Query Match           5.1%;    Score 113.5; DB 5; Length 128;
    Best Local Similarity  26.4%;  Pred. No. 0.44;
RESULT 910
ID  AAW64359 standard; protein; 267 AA.
DE  Mycobacterium tuberculosis antigen TbH-29.
PN  WO9816645-A2.
PD  23-APR-1998.
PA  (CORI-) CORIXA CORP.
    Query Match           5.1%;    Score 113.5; DB 2; Length 267;
    Best Local Similarity  27.5%;  Pred. No. 1.2;
RESULT 911
ID  AAW81726 standard; protein; 267 AA.
DE  M. tuberculosis immunogenic polypeptide TbH-29.
PN  WO9816646-A2.
PD  23-APR-1998.
PA  (CORI-) CORIXA CORP.
    Query Match           5.1%;    Score 113.5; DB 2; Length 267;
    Best Local Similarity  27.5%;  Pred. No. 1.2;
RESULT 912
ID  AAY39013 standard; protein; 267 AA.
DE  M. tuberculosis recombinant antigen protein TbH-29.
PN  WO9942118-A2.
PD  26-AUG-1999.
PA  (CORI-) CORIXA CORP.
    Query Match           5.1%;    Score 113.5; DB 2; Length 267;
    Best Local Similarity  27.5%;  Pred. No. 1.2;
RESULT 913
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ID   AAY39156 standard; protein; 267 AA.
DE   M. tuberculosis antigen TBH-29 amino acid sequence.
PN   WO9942076-A2.
PD   26-AUG-1999.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5; DB 2; Length 267;
     Best Local Similarity 27.5%;   Pred. No. 1.2;

RESULT 914
ID   AAM39027 standard; protein; 378 AA.
DE   Human polypeptide SEQ ID NO 2172.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.1%;   Score 113.5; DB 4; Length 378;
     Best Local Similarity 25.1%;   Pred. No. 2;

RESULT 915
ID   ABU42529 standard; protein; 469 AA.
DE   Protein encoded by Prokaryotic essential gene #28056.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.1%;   Score 113.5; DB 6; Length 469;
     Best Local Similarity 18.6%;   Pred. No. 2.8;

RESULT 916
ID   AAB61923 standard; protein; 505 AA.
DE   Human early growth response factor-1 (Egr-1).
PN   WO200104356-A1.
PD   18-JAN-2001.
PA   (GENE-) GENE LOGIC INC.
     Query Match   5.1%;   Score 113.5; DB 4; Length 505;
     Best Local Similarity 22.2%;   Pred. No. 3.1;

RESULT 917
ID   AAR24022 standard; protein; 543 AA.
DE   Human promyelo-leukaemia cell HL-20 differentiation protein.
PN   JP04121189-A.
PD   22-APR-1992.
PA   (TOYJ) TOSOH CORP.
PA   (UCHI/) UCHIYAMA T.
     Query Match   5.1%;   Score 113.5; DB 2; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4

RESULT 918
ID   AAW76985 standard; protein; 543 AA.
DE   Human EGR-1 protein.
PN   US5837692-A.
PD   17-NOV-1998.
PA   (ADAM/) ADAMSON E.
PA   (MERC/) MERCOLA D.
     Query Match   5.1%;   Score 113.5; DB 3; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 919
ID   AAY51116 standard; protein; 543 AA.
DE   Human EGR-1 protein.
PN   US6008048-A.
PD   28-DEC-1999.
PA   (ISIS-) ISIS PHARM INC.
     Query Match   5.1%;   Score 113.5; DB 4; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 920
ID   AAU09066 standard; protein; 543 AA.
DE   Human ZIF268 protein.
PN   WO200174298-A2.
PD   11-OCT-2001.
PA   (UYBR-) UNIV BROWN RESEACH FOUND.
     Query Match   5.1%;   Score 113.5; DB 4; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 921
ID   AAB76861 standard; protein; 543 AA.
DE   Human lung tumour protein related protein sequence SEQ ID NO:337.
PN   WO200100828-A2.
PD   04-JAN-2001.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5; DB 4; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 922
ID   AAU85516 standard; protein; 543 AA.
DE   Clone #18996 of lung tumour protein.
PN   WO200204514-A2.
PD   17-JAN-2002.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5; DB 5; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 923
ID   ABU69488 standard; protein; 543 AA.
DE   Human lung cancer associated cDNA #18996 protein.
PN   US2002197669-A1.
PD   26-DEC-2002.
PA   (BANG/) BANGUR C S.
PA   (FANG/) FANGER G R.
PA   (WANG/) WANG A.
PA   (WANG/) WANG T.
PA   (SWIT/) SWITZER A P.
PA   (MCNE/) MCNEILL P D.
PA   (CLAP/) CLAPPER J D.
     Query Match   5.1%;   Score 113.5; DB 6; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 924
ID   ABU66390 standard; protein; 543 AA.
DE   Lung cancer therapy and diagnosis associated protein #14.
PN   US2002172952-A1.
PD   21-NOV-2002.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5; DB 6; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 925
ID   ADB75271 standard; protein; 543 AA.
DE   Prostate cancer marker protein.
PN   WO2003009814-A2.
PD   06-FEB-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   5.1%;   Score 113.5; DB 7; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 926
ID   ADC37141 standard; protein; 543 AA.
DE   543 amino acid Egr-1 human protein.
PN   WO2003060516-A1.
PD   24-JUL-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.1%;   Score 113.5; DB 7; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 927
ID   ADD48114 standard; protein; 543 AA.
DE   Human Protein NP_001955, SEQ ID NO 13812.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.1%;   Score 113.5; DB 7; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 928
ID   ADH45856 standard; protein; 543 AA.
DE   Human lung tumour clone protein, SEQ ID No 337.
PN   WO2003037267-A2.
PD   08-MAY-2003.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5; DB 7; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 929
ID   ADE71608 standard; protein; 543 AA.
DE   Human lung tumour protein #14.
PN   US2003125245-A1.
PD   03-JUL-2003.
PA   (WANG/) WANG T.
PA   (BANG/) BANGUR C S.
     Query Match   5.1%;   Score 113.5; DB 8; Length 543;
     Best Local Similarity 22.2%;   Pred. No. 3.4;

RESULT 930
ID   ADO24391 standard; protein; 543 AA.
DE   Human PRO37335 protein SEQ ID NO:30.
PN   WO2004043397-A2.
PD   27-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 8;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 931
ID   ADO20423 standard; protein; 543 AA.
DE   Human PRO polypeptide #656.
PN   WO2004043361-A2.
PD   27-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 8;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 932
ID   ADJ19775 standard; protein; 543 AA.
DE   Human lung cancer-related protein - SEQ ID 337.
PN   US2003211510-A1.
PD   13-NOV-2003.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5;   DB 8;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 933
ID   ABM80651 standard; protein; 543 AA.
DE   Tumour-associated antigenic target (TAT) polypeptide PRO37335, SEQ:1690.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 8;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 934
ID   ADP54278 standard; protein; 543 AA.
DE   Human PRO protein sequence SEQ ID NO:254.
PN   WO2004039956-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 8;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 935
ID   ADY18712 standard; protein; 543 AA.
DE   PRO polypeptide SEQ ID NO 4518.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 936
ID   ADY19630 standard; protein; 543 AA.
DE   PRO polypeptide SEQ ID NO 5436.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 937
ID   AEA23530 standard; protein; 543 AA.
DE   Human PRO polypeptide SEQ ID NO 72.
PN   WO2005051988-A2.
PD   09-JUN-2005.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 938
ID   ABD07142 standard; protein; 543 AA.
DE   Respiratory disease-associated protein, EGR1.
PN   WO2005092383-A1.
PD   06-OCT-2005.
PA   (TAKE) TAKEDA PHARM CO LTD.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 939

ID   AEE18753 standard; protein; 543 AA.
DE   Human early growth response factor-1 (Egr-1) protein, SEQ ID NO: 3.
PN   US6969704-B1.
PD   29-NOV-2005.
PA   (UYCO) UNIV COLUMBIA NEW YORK.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 940
ID   AEE18755 standard; protein; 543 AA.
DE   Human early growth response factor-1 (Egr-1) protein, SEQ ID NO: 5.
PN   US6969704-B1.
PD   29-NOV-2005.
PA   (UYCO) UNIV COLUMBIA NEW YORK.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 941
ID   AEH22433 standard; protein; 543 AA.
DE   Human lung tumor associated protein, SEQ ID 337.
PN   US2006088527-A1.
PD   27-APR-2006.
PA   (CORI-) CORIXA CORP.
     Query Match   5.1%;   Score 113.5;   DB 10;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 942
ID   AEJ10602 standard; protein; 543 AA.
DE   Mouse transcription factor Zif268 protein.
PN   US2006154240-A1.
PD   13-JUL-2006.
PA   (IOWA) UNIV IOWA STATE RES FOUND INC.
     (IOWA) UNIV IOWA RES FOUND.
     Query Match   5.1%;   Score 113.5;   DB 10;   Length 543;
     Best Local Similarity 22.2%; Pred. No. 3.4;
RESULT 943
ID   ADM40792 standard; protein; 548 AA.
DE   Mycobacterial disease detection method related Rv0538 protein.
PN   WO2003073101-A2.
PD   04-SEP-2003.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.1%;   Score 113.5;   DB 7;   Length 548;
     Best Local Similarity 27.5%; Pred. No. 3.5;
RESULT 944
ID   AEB91614 standard; protein; 548 AA.
DE   Microbial pathogen adhesin protein sequence, SEQ ID NO:324.
PN   WO2005076010-A2.
PD   18-AUG-2005.
PA   (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.
     Query Match   5.1%;   Score 113.5;   DB 9;   Length 548;
     Best Local Similarity 27.5%; Pred. No. 3.5;
RESULT 945
ID   AEL00855 standard; protein; 596 AA.
DE   Mucin-like protein associated polypeptide SEQ ID NO 171.
PN   WO2006082851-A1.
PD   10-AUG-2006.
PA   (UYTY) UNIV TOKYO.
     Query Match   5.1%;   Score 113.5;   DB 10;   Length 596;
     Best Local Similarity 25.5%; Pred. No. 3.9;
RESULT 946
ID   AEL00859 standard; protein; 596 AA.
DE   Mucin-like protein associated polypeptide SEQ ID NO 175.
PN   WO2006082851-A1.
PD   10-AUG-2006.
PA   (UYTY) UNIV TOKYO.
     Query Match   5.1%;   Score 113.5;   DB 10;   Length 596;
     Best Local Similarity 25.5%; Pred. No. 3.9;
RESULT 947
ID   ADN20575 standard; protein; 1103 AA.
DE   Bacterial polypeptide #3228.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.

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PA  (GOLD/) GOLDMAN B S.
    Query Match         5.1%;   Score 113.5;  DB 8;  Length 1103;
    Best Local Similarity  25.7%;   Pred. No. 9.3;
RESULT 948
ID  ABB65879 standard; protein; 307 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match         5.1%;   Score 113;  DB 4;  Length 307;
    Best Local Similarity  29.1%;   Pred. No. 1.7;
RESULT 949
ID  AEF57533 standard; protein; 393 AA.
DE  Yeast p62 nucleoporin 1 to 392 amino acid sequence SEQ ID NO:1.
PN  US2006035823-A1.
PD  16-FEB-2006.
PA  (LEDE/) LEDERMAN S.
PA  (GAMP/) GAMPER C.
RESULT 950
ID  AAU27715 standard; protein; 415-AA.
DE  Human full-length polypeptide sequence #40.
PN  WO200164834-A2.
PD  07-SEP-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match         5.1%;   Score 113;  DB 4;  Length 415;
    Best Local Similarity  24.3%;   Pred. No. 2.6;
RESULT 951
ID  AAB31195 standard; protein; 482 AA.
DE  Amino acid sequence of human polypeptide PRO7170.
PN  WO200077037-A2.
PD  21-DEC-2000.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 4;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 952
ID  AAB27225 standard; protein; 482 AA.
DE  Human EXMAD-3 SEQ ID NO: 3.
PN  WO200068380-A2.
PD  16-NOV-2000.
PA  (INCY-) INCYTE GENOMICS INC.
    Query Match         5.1%;   Score 113;  DB 4;  Length 482;
    Best Local Similarity  24.3%;   Pred. No. 2.6;
RESULT 953
ID  AAY97586 standard; protein; 482 AA.
DE  Human secreted protein PRO7170.
PN  WO200075317-A2.
PD  14-DEC-2000.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 4;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 954
ID  AAB65298 standard; protein; 482 AA.
DE  Human PRO7170 protein sequence SEQ ID NO:513.
PN  WO200073454-A1.
PD  07-DEC-2000.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 4;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 955
ID  ABU58113 standard; protein; 482 AA.
DE  Human PRO polypeptide #145.
PN  US2003027163-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 956
ID  ABU59191 standard; protein; 482 AA.
DE  Novel human secreted or transmembrane protein PRO7170.
PN  US2002132252-A1.
PD  19-SEP-2002.
PA  (GETH ) GENENTECH INC.

    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 957
ID  ABU82703 standard; protein; 482 AA.
DE  Human secreted/transmembrane protein PRO7170.
PN  US2003032023-A1.
PD  13-FEB-2003.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 958
ID  ABU60622 standard; protein; 482 AA.
DE  Human secreted/transmembrane protein, #181.
PN  US2002160384-A1.
PD  31-OCT-2002.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 959
ID  ABO25166 standard; protein; 482 AA.
DE  Novel human secreted and transmembrane protein PRO7170.
PN  US2003040014-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 960
ID  ABU14004 standard; protein; 482 AA.
DE  Human PRO7170 polypeptide.
PN  US2002103125-A1.
PD  01-AUG-2002.
PA  (GETH ) GENENTECH LTD.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 961
ID  ABU72589 standard; protein; 482 AA.
DE  Novel human secreted and transmembrane protein PRO7170.
PN  US2003303531-A1.
PD  02-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 962
ID  ABU67284 standard; protein; 482 AA.
DE  Novel human secreted and transmembrane protein PRO7170.
PN  US2003032063-A1.
PD  13-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 963
ID  ABU59338 standard; protein; 482 AA.
DE  Human secreted/transmembrane protein, #181.
PN  US2003027162-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 964
ID  ABO26035 standard; protein; 482 AA.
DE  Human PRO7170 polypeptide.
PN  US2002127576-A1.
PD  12-SEP-2002.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 965
ID  ABU72052 standard; protein; 482 AA.
DE  Novel human secreted and transmembrane protein PRO7170.
PN  US2002177165-A1.
PD  28-NOV-2002.
PA  (GETH ) GENENTECH INC.
    Query Match         5.1%;   Score 113;  DB 6;  Length 482;
    Best Local Similarity  23.0%;   Pred. No. 3.2;
RESULT 966
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ID   ABU67153 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 967
ID   ABU59044 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein, #181.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 968
ID   ABU92422 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003022187-A1.
PD   30-JAN-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 969
ID   ABU59487 standard; protein; 482 AA.
DE   Novel human secreted or transmembrane protein PRO361.
PN   US2003027985-A1.
PD   06-FEB-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 970
ID   ABU92253 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003017476-A1.
PD   23-JAN-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 971
ID   ABU10959 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 972
ID   ABU81711 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2002177164-A1.
PD   28-NOV-2002.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 973
ID   ABU79795 standard; protein; 482 AA.
DE   Human secreted/transmembrane polypeptide PRO7170.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 974
ID   ABU88650 standard; protein; 482 AA.
DE   Human secreted and transmembrane protein PRO7170.
PN   US2002197615-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 975
ID   ABO34164 standard; protein; 482 AA.
DE   Human PRO7170 polypeptide.
PN   US2003017981-A1.
PD   23-JAN-2003.

     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 976
ID   ADA38024 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 977
ID   ADA21710 standard; protein; 482 AA.
DE   Human secreted/transmembrane polypeptide PRO7170.
PN   US2003054404-A1.
PD   20-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 978
ID   ADA10497 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein, PRO7170.
PN   US2003059831-A1.
PD   27-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 979
ID   ADA18041 standard; protein; 482 AA.
DE   Human PRO7170 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 980
ID   ADA28149 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003054359-A1.
PD   20-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 981
ID   ADA47235 standard; protein; 482 AA.
DE   Human secreted/transmembrane polypeptide PRO7470.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 982
ID   ADA94729 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003059832-A1.
PD   27-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 983
ID   ADA38954 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003059780-A1.
PD   27-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 984
ID   ADA93075 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003060407-A1.
PD   27-MAR-2003.
     Query Match   5.1%; Score 113; DB 6; Length 482;
     Best Local Similarity   23.0%; Pred. No. 3.2;
RESULT 985
ID   ABO53250 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003044806-A1.
PD   06-MAR-2003.
     Query Match   5.1%; Score 113; DB 7; Length 482;

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     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 986
ID   ADA22636 standard; protein; 482 AA.
DE   Human secreted/transmembrane polypeptide PRO7170.
PN   US2003040473-A1.
PD   27-FEB-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 987
ID   ABO22620 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003017982-A1.
PD   23-JAN-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 988
ID   ABO19853 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003044902-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 989
ID   ADA06802 standard; protein; 482 AA.
DE   Human secreted/transmembrane PRO polypeptide #145.
PN   US2003049638-A1.
PD   13-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 990
ID   ADA39495 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003059782-A1.
PD   27-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 991
ID   ADB96521 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003054403-A1.
PD   20-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 992
ID   ADC57993 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003027754-A1.
PD   06-FEB-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 993
ID   ADC55357 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003045463-A1.
PD   06-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 994
ID   ADC12224 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003049681-A1.
PD   13-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 995
ID   ADC56646 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003064375-A1.
PD   03-APR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 996

ID   ADC11691 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003069403-A1.
PD   10-APR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 997
ID   ADC14813 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003082546-A1.
PD   01-MAY-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 998
ID   ADD08345 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003068623-A1.
PD   10-APR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 999
ID   ADC82170 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003083461-A1.
PD   01-MAY-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1000
ID   ADD07812 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1001
ID   ADC82703 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003059833-A1.
PD   27-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1002
ID   ADD08883 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003073090-A1.
PD   17-APR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1003
ID   ADD07132 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1004
ID   ADC83379 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003059783-A1.
PD   27-MAR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1005
ID   ADD55486 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003077593-A1.
PD   24-APR-2003.
     Query Match    5.1%;   Score 113; DB 7;   Length 482;
     Best Local Similarity    23.0%;   Pred. No. 3.2;
RESULT 1006
ID   ADD56444 standard; protein; 482 AA.
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DE   Human PRO polypeptide #145.
PN   US2003077594-A1.
PD   24-APR-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1007
ID   ADD54882 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1008
ID   ADE31901 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003068647-A1.
PD   10-APR-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1009
ID   ADE27036 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003087304-A1.
PD   08-MAY-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1010
ID   ADE26503 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003087305-A1.
PD   08-MAY-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1011
ID   ADF67440 standard; protein; 482 AA.
DE   Human PRO7170 amino acid sequence SEQ ID NO:513.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1012
ID   ADG63744 standard; protein; 482 AA.
DE   Human secreted/transmembrane polypeptide PRO7470.
PN   US2003170721-A1.
PD   11-SEP-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1013
ID   ADI35694 standard; protein; 482 AA.
DE   Human PRO polypeptide #145.
PN   US2003050457-A1.
PD   13-MAR-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1014
ID   ADI00187 standard; protein; 482 AA.
DE   Novel human secreted and transmembrane protein PRO7170.
PN   US2003049682-A1.
PD   13-MAR-2003.
     Query Match     5.1%;   Score 113;  DB 7;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1015
ID   ADE41158 standard; protein; 482 AA.
DE   Human secreted/transmembrane polypeptide PRO7470.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1016


ID   ADF35639 standard; protein; 482 AA.
DE   Human PRO7170 polypeptide.
PN   US2003194760-A1.
PD   16-OCT-2003.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1017
ID   ADG11889 standard; protein; 482 AA.
DE   Human PRO7170 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1018
ID   ADH19759 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1019
ID   ADG63593 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1020
ID   ADH21252 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003224358-A1.
PD   04-DEC-2003.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1021
ID   ADH20292 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein PRO7170.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 8;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1022
ID   AEA38661 standard; protein; 482 AA.
DE   Human secreted/transmembrane protein, #213.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH ) GENENTECH INC.
     Query Match     5.1%;   Score 113;  DB 9;   Length 482;
     Best Local Similarity   23.0%;   Pred. No. 3.2;
RESULT 1023
ID   AAB20165 standard; protein; 503 AA.
DE   Human protein associated with IgA nephropathy.
PN   WO200105803-A1.
PD   25-JAN-2001.
PA   (GENE-) GENE LOGIC INC.
     Query Match     5.1%;   Score 113;  DB 4;   Length 503;
     Best Local Similarity   23.0%;   Pred. No. 3.4;
RESULT 1024
ID   ADB61537 standard; protein; 503 AA.
DE   Hepatocyte growth factor (HGF) receptor related protein, SEQ ID No 10.
PN   WO2003053467-A1.
PD   03-JUL-2003.
PA   (NISB ) JAPAN TOBACCO INC.
     Query Match     5.1%;   Score 113;  DB 7;   Length 503;
     Best Local Similarity   23.0%;   Pred. No. 3.4;
RESULT 1025
ID   ADD47883 standard; protein; 522 AA.
DE   Human Protein NP_057637, SEQ ID NO 13579.
PN   WO2003016475-A2.
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PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match        5.1%;    Score 113;   DB 7;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1026
ID   ADE61833 standard; protein; 522 AA.
DE   Human Protein P37198, SEQ ID NO 7761.
PN   WO200301647S-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match        5.1%;    Score 113;   DB 7;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1027
ID   ADL83001 standard; protein; 522 AA.
DE   Human PRO84695, SEQ ID 203.
PN   WO200402409S-A2.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        5.1%;    Score 113;   DB 8;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1028
ID   ADP54326 standard; protein; 522 AA.
DE   Human PRO protein sequence SEQ ID NO:302.
PN   WO200403995G-A2.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        5.1%;    Score 113;   DB 8;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1029
ID   ADX07439 standard; protein; 522 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 2004.
PN   WO200501287S-A2.
PD   10-FEB-2005.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
     Query Match        5.1%;    Score 113;   DB 9;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1030
ID   ADX07437 standard; protein; 522 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 2002.
PN   WO200501287S-A2.
PD   10-FEB-2005.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
     Query Match        5.1%;    Score 113;   DB 9;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1031
ID   ADX07441 standard; protein; 522 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 2006.
PN   WO200501287S-A2.
PD   10-FEB-2005.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
     Query Match        5.1%;    Score 113;   DB 9;   Length 522;
     Best Local Similarity  24.3%;    Pred. No. 3.5;
RESULT 1032
ID   AAE06598 standard; protein; 538 AA.
DE   Human protein having hydrophobic domain, HP10775.
PN   WO200147728-A2.
PD   12-JUL-2001.
PA   (PROT-) PROTEGENE INC.
PA   (SAGA ) SAGAMI CHEM RES CENT.
     Query Match        5.1%;    Score 113;   DB 4;   Length 538;
     Best Local Similarity  23.0%;    Pred. No. 3.7;
RESULT 1033
ID   AAM38985 standard; protein; 538 AA.
DE   Human polypeptide SEQ ID NO 2130.
PN   WO20015331Z-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match        5.1%;    Score 113;   DB 4;   Length 538;
     Best Local Similarity  23.0%;    Pred. No. 3.7;
RESULT 1034
ID   AAM40771 standard; protein; 561 AA.
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DE   Human polypeptide SEQ ID NO 5702.
PN   WO20015331Z-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match        5.1%;    Score 113;   DB 4;   Length 561;
     Best Local Similarity  23.3%;    Pred. No. 3.9;
RESULT 1035
ID   AAE00708 standard; protein; 681 AA.
DE   Marburg virus Ravn strain glycoprotein (GP).
PN   US6200959-B1.
PD   13-MAR-2001.
PA   (POWD-) POWDERJECT VACCINES INC.
     Query Match        5.1%;    Score 113;   DB 4;   Length 681;
     Best Local Similarity  23.9%;    Pred. No. 5.2;
RESULT 1036
ID   AEH93671 standard; protein; 714 AA.
DE   C. glabrata Epa7 protein.
PN   WO20060592Z8-A2.
PD   08-JUN-2006.
PA   (INSP ) INST PASTEUR.
     Query Match        5.1%;    Score 113;   DB 10;   Length 714;
     Best Local Similarity  20.5%;    Pred. No. 5.5;
RESULT 1037
ID   ABG04814 standard; protein; 729 AA.
DE   Novel human diagnostic protein #4805.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match        5.1%;    Score 113;   DB 4;   Length 729;
     Best Local Similarity  19.8%;    Pred. No. 5.7;
RESULT 1038
ID   AAW29666 standard; protein; 772 AA.
DE   Homo sapiens DH1308_1 clone secreted protein.
PN   WO983069S-A2.
PD   16-JUL-1998.
PA   (GEMY ) GENETICS INST INC.
     Query Match        5.1%;    Score 113;   DB 2;   Length 772;
     Best Local Similarity  20.0%;    Pred. No. 6.2;
RESULT 1039
ID   ABP73285 standard; protein; 841 AA.
DE   Candida albicans essential protein SEQ ID NO 7122.
PN   WO20025372B-A2.
PD   11-JUL-2002.
PA   (ELIR-) ELITRA PHARM INC.
     Query Match        5.1%;    Score 113;   DB 5;   Length 841;
     Best Local Similarity  20.5%;    Pred. No. 7;
RESULT 1040
ID   AAR60563 standard; protein; 862 AA.
DE   Yeast 2.6 kB agglutination gene FLO1S.
PN   WO941947S-A2.
PD   01-SEP-1994.
PA   (SAPB ) SAPPORO BREWERIES.
PA   (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
     Query Match        5.1%;    Score 113;   DB 2;   Length 862;
     Best Local Similarity  20.4%;    Pred. No. 7.2;
RESULT 1041
ID   AAR58754 standard; protein; 894 AA.
DE   S. cerevisiae FLO1.
PN   WO9418330-A1.
PD   18-AUG-1994.
PA   (UNIL ) UNILEVER PLC.
PA   (UNIL ) UNILEVER NV.
     Query Match        5.1%;    Score 113;   DB 2;   Length 894;
     Best Local Similarity  20.4%;    Pred. No. 7.6;
RESULT 1042
ID   AAR47578 standard; protein; 894 AA.
DE   Flocculation protein of Saccharomyces cerevisiae.
PN   WO940156Z-A1.
PD   20-JAN-1994.
PA   (UNIL ) UNILEVER PLC.
PA   (UNIL ) UNILEVER NV.
     Query Match        5.1%;    Score 113;   DB 2;   Length 894;
     Best Local Similarity  20.4%;    Pred. No. 7.6;
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RESULT 1043
ID   ABB63615 standard; protein; 916 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 17637.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
   Query Match   5.1%;   Score 113; DB 4; Length 916;
   Best Local Similarity 24.3%;   Pred. No. 7.9;
RESULT 1044
ID   AD001008 standard; protein; 916 AA.
DE   Fruit fly AD-related protein CG7983 (Guanylate kinase).
PN   US2004067535-A1.
PD   08-APR-2004.
PA   (LIFE-) LIFE SCI DEV CORP.
   Query Match   5.1%;   Score 113; DB 8; Length 916;
   Best Local Similarity 24.3%;   Pred. No. 7.9;
RESULT 1045
ID   ADS96718 standard; protein; 916 AA.
DE   Drosophila melanogaster protein, SEQ ID 339.
PN   WO2004039999-A2.
PD   13-MAY-2004.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
   Query Match   5.1%;   Score 113; DB 8; Length 916;
   Best Local Similarity 24.3%;   Pred. No. 7.9;
RESULT 1046
ID   ADW07662 standard; protein; 984 AA.
DE   Human MPTEN polypeptide #15.
PN   WO2005003297-A2.
PD   13-JAN-2005.
PA   (EXEL-) EXELIXIS INC.
   Query Match   5.1%;   Score 113; DB 9; Length 984;
   Best Local Similarity 20.9%;   Pred. No. 8.7;
RESULT 1047
ID   ADX07652 standard; protein; 984 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 2217.
PN   WO2005012875-A2.
PD   10-FEB-2005.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
   Query Match   5.1%;   Score 113; DB 9; Length 984;
   Best Local Similarity 20.9%;   Pred. No. 8.7;
RESULT 1048
ID   ADJ70227 standard; protein; 999 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID2033.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
   Query Match   5.1%;   Score 113; DB 7; Length 999;
   Best Local Similarity 20.9%;   Pred. No. 8.9;
RESULT 1049
ID   AAR60562 standard; protein; 1537 AA.
DE   Yeast 4.7 kB agglutination gene FLO1L.
PN   WO941994/5-A2.
PD   01-SEP-1994.
PA   (SAPB) SAPPORO BREWERIES.
PA   (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
   Query Match   5.1%;   Score 113; DB 2; Length 1537;
   Best Local Similarity 20.4%;   Pred. No. 16;
RESULT 1050
ID   ADP87475 standard; protein; 1537 AA.
DE   S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN   WO2004057033-A1.
PD   08-JUL-2004.
PA   (ROSE-) ROSETTA INPHARMATICS LLC.
   Query Match   5.1%;   Score 113; DB 8; Length 1537;
   Best Local Similarity 20.4%;   Pred. No. 16;
RESULT 1051
ID   ADN18745 standard; protein; 1537 AA.
DE   Bacterial polypeptide #1398.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.

PA   (SLAT/) SLATER S C.
PA   (CHEN//) CHEN X.
PA   (GOLD/) GOLDMAN B S.
   Query Match   5.1%;   Score 113; DB 8; Length 1537;
   Best Local Similarity 20.4%;   Pred. No. 16;
RESULT 1052
ID   ABP69142 standard; protein; 1759 AA.
DE   Human polypeptide SEQ ID NO 1189.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSE-) HYSEQ INC.
   Query Match   5.1%;   Score 113; DB 5; Length 1759;
   Best Local Similarity 19.0%;   Pred. No. 20;
RESULT 1053
ID   AAB97070 standard; protein; 2058 AA.
DE   Human polypeptide #3 expressed in intraabdominal adipose tissue.
PN   JP2001008699-A.
PD   16-JAN-2001.
PA   (SUMO) SUMITOMO CHEM CO LTD.
   Query Match   5.1%;   Score 113; DB 4; Length 2058;
   Best Local Similarity 23.0%;   Pred. No. 25;
RESULT 1054
ID   ADX07779 standard; protein; 2090 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 2344.
PN   WO2005012875-A2.
PD   10-FEB-2005.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
   Query Match   5.1%;   Score 113; DB 9; Length 2090;
   Best Local Similarity 23.0%;   Pred. No. 25;
RESULT 1055
ID   AEF58534 standard; protein; 2090 AA.
DE   Human nucleoporin NUP214.
PN   WO2006005153-A1.
PD   19-JAN-2006.
PA   (BCCA-) BC CANCER AGENCY.
PA   (UYMO-) UNIV MONTREAL.
   Query Match   5.1%;   Score 113; DB 10; Length 2090;
   Best Local Similarity 23.0%;   Pred. No. 25;
RESULT 1056
ID   ADF09542 standard; protein; 2127 AA.
DE   Human nucleoporin 214kDa protein SEQ ID NO:43.
PN   WO2003066940-A2.
PD   21-AUG-2003.
PA   (CURA-) CURAGEN CORP.
PA   (HOFF) HOFFMANN LA ROCHE INC.
   Query Match   5.1%;   Score 113; DB 7; Length 2127;
   Best Local Similarity 23.0%;   Pred. No. 25;
RESULT 1057
ID   ADX07781 standard; protein; 2130 AA.
DE   Cyclin-dependent kinase modulation biomarker SEQ ID NO 2346.
PN   WO2005012875-A2.
PD   10-FEB-2005.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
   Query Match   5.1%;   Score 113; DB 9; Length 2130;
   Best Local Similarity 23.0%;   Pred. No. 26;
RESULT 1058
ID   AAM40813 standard; protein; 233 AA.
DE   Human polypeptide SEQ ID NO 5744.
PN   WO20015312-A1.
PD   26-JUL-2001.
PA   (HYSB-) HYSEQ INC.
   Query Match   5.1%;   Score 112.5; DB 4; Length 233;
   Best Local Similarity 25.1%;   Pred. No. 1.2;
RESULT 1059
ID   ADX67250 standard; protein; 269 AA.
DE   Plant full length insert polypeptide seqid 38093.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.

PA   (CAOY/) CAO Y.
     Query Match   5.1%; Score 112.5; DB 8; Length 269;
     Best Local Similarity   26.9%; Pred. No. 1.5;
RESULT 1060
ID   ADA50571 standard; protein; 307 AA.
DE   Mucin 1 (MUC-1) splice variant #1, SEQ ID NO:26.
PN   WO200301569-A2.
PD   17-APR-2003.
PA   (CENZ) CENTOCOR INC.
     Query Match   5.1%; Score 112.5; DB 6; Length 307;
     Best Local Similarity   28.3%; Pred. No. 1.8;
RESULT 1061
ID   ADU49609 standard; protein; 307 AA.
DE   Human mucin-1 (MUC1) polypeptide.
PN   WO2004096238-A1.
PD   11-NOV-2004.
PA   (CENZ) CENTOCOR INC.
PA   (GOLE/) GOLETZ T J.
PA   (MCCA/) MCCARTHY S G.
PA   (SCAL/) SCALLON B J.
PA   (SNYD/) SNYDER L A.
PA   (BRAN/) BRANIGAN P J.
     Query Match   5.1%; Score 112.5; DB 8; Length 307;
     Best Local Similarity   28.3%; Pred. No. 1.8;
RESULT 1062
ID   AAM16316 standard; protein; 331 AA.
DE   Peptide #2750 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1063
ID   ABB35308 standard; peptide; 331 AA.
DE   Peptide #2814 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1064
ID   AAM28811 standard; protein; 331 AA.
DE   Peptide #2848 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1065
ID   ABB30138 standard; peptide; 331 AA.
DE   Peptide #2789 encoded by breast cell single exon nucleic acid probe.
PN   WO200157271-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1066
ID   ABB20750 standard; protein; 331 AA.
DE   Protein #2749 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1067
ID   AAM68512 standard; protein; 331 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 28818.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1068

ID   AAM56139 standard; protein; 331 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 28244.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1069
ID   ABG50181 standard; peptide; 331 AA.
DE   Human liver peptide, SEQ ID No 28829.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1070
ID   AAM04054 standard; protein; 331 AA.
DE   Peptide #2736 encoded by probe for measuring breast gene expression.
PN   WO200157270-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 4; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1071
ID   ABG38093 standard; peptide; 331 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 27758.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match   5.1%; Score 112.5; DB 5; Length 331;
     Best Local Similarity   26.3%; Pred. No. 2;
RESULT 1072
ID   ABP70436 standard; protein; 345 AA.
DE   Amino acid sequence of murine TIM-4 BALB/c allele.
PN   WO2003002722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.1%; Score 112.5; DB 6; Length 345;
     Best Local Similarity   21.7%; Pred. No. 2.2;
RESULT 1073
ID   ADY98067 standard; protein; 345 AA.
DE   Mouse TIM-4.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
PA   (DAND) DANA FARBER CANCER INST INC.
     Query Match   5.1%; Score 112.5; DB 9; Length 345;
     Best Local Similarity   21.7%; Pred. No. 2.2;
RESULT 1074
ID   AED60511 standard; protein; 345 AA.
DE   Mouse TIM-4 protein SEQ ID NO:19.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
     Query Match   5.1%; Score 112.5; DB 9; Length 345;
     Best Local Similarity   21.7%; Pred. No. 2.2;
RESULT 1075
ID   ABP70446 standard; protein; 378 AA.
DE   Amino acid sequence of human TIM-4 allele 1.
PN   WO2003002722-A2.
PD   09-JAN-2003.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
     Query Match   5.1%; Score 112.5; DB 6; Length 378;
     Best Local Similarity   25.1%; Pred. No. 2.5;
RESULT 1076
ID   ADY98087 standard; protein; 378 AA.
DE   Human TIM-4 allele 1-encoded protein.
PN   WO2005027854-A2.
PD   31-MAR-2005.
PA   (STRD) UNIV LELAND STANFORD JUNIOR.
PA   (DAND) DANA FARBER CANCER INST INC.
     Query Match   5.1%; Score 112.5; DB 9; Length 378;
     Best Local Similarity   25.1%; Pred. No. 2.5;

RESULT 1077
ID   AED01585 standard; protein; 378 AA.
DE   Human tim-4 polypeptide variant #1.
PN   WO2005090573-A2.
PD   29-SEP-2005.
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
     Query Match   5.1%; Score 112.5; DB 9; Length 378;
     Best Local Similarity   25.1%; Pred. No. 2.5;
RESULT 1078
ID   AED01593 standard; protein; 378 AA.
DE   Human soluble tim-4 polypeptide.
PN   WO2005090573-A2.
PD   29-SEP-2005.
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
     Query Match   5.1%; Score 112.5; DB 9; Length 378;
     Best Local Similarity   25.1%; Pred. No. 2.5;
RESULT 1079
ID   AED60531 standard; protein; 378 AA.
DE   Human TIM-3, allele 4, protein SEQ ID NO:39.
PN   WO2005097211-A2.
PD   20-OCT-2005.
PA   (TELO-) TELOS PHARM INC.
     Query Match   5.1%; Score 112.5; DB 9; Length 378;
     Best Local Similarity   25.1%; Pred. No. 2.5;
RESULT 1080
ID   AAY25768 standard; protein; 379 AA.
DE   Human secreted protein encoded from gene 58.
PN   WO9938881-A1.
PD   05-AUG-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   5.1%; Score 112.5; DB 2; Length 379;
     Best Local Similarity   25.1%; Pred. No. 2.5;
RESULT 1081
ID   ADX90096 standard; protein; 545 AA.
DE   Plant full length insert polypeptide seqid 52760.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   5.1%; Score 112.5; DB 8; Length 545;
     Best Local Similarity   20.1%; Pred. No. 4.1;
RESULT 1082
ID   ABU96715 standard; protein; 612 AA.
DE   Human nucleic acid-associated protein (NAAP) #44.
PN   WO2003023003-A2.
PD   20-MAR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   5.1%; Score 112.5; DB 6; Length 612;
     Best Local Similarity   23.3%; Pred. No. 4.9;
RESULT 1083
ID   AAB92955 standard; protein; 676 AA.
DE   Human protein sequence SEQ ID NO:11640.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
     Query Match   5.1%; Score 112.5; DB 4; Length 676;
     Best Local Similarity   21.8%; Pred. No. 5.6;
RESULT 1084
ID   AEK18311 standard; protein; 696 AA.
DE   Human KIAA0916 protein, PAM.g.
PN   US20062204503-A1.
PD   14-SEP-2006.
PA   (BIOJ) BIOGEN IDEC MA INC.
     Query Match   5.1%; Score 112.5; DB 10; Length 696;
     Best Local Similarity   25.5%; Pred. No. 5.9;
RESULT 1085
ID   ADJ80141 standard; protein; 807 AA.

DE   Novel human nucleic acid-associated protein #17.
PN   WO2003038052-A2.
PD   08-MAY-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   5.1%; Score 112.5; DB 7; Length 807;
     Best Local Similarity   21.8%; Pred. No. 7.2;
RESULT 1086
ID   AEC20243 standard; protein; 807 AA.
DE   Human nucleic acid-associated protein (NAAP) - SEQ ID 17.
PN   US2005186569-A1.
PD   25-AUG-2005.
PA   (BECH/) BECHA S D.
PA   (BORO/) BOROWSKY M L.
PA   (BURF/) BURFORD N.
PA   (CHAW/) CHAWLA N K.
PA   (ELLI/) ELLIOTT V S.
PA   (EMER/) EMERLING B M.
PA   (FORS/) FORSYTHE I J.
PA   (GIET/) GIETZEN K J.
PA   (GORV/) GORVAD A E.
PA   (GRIF/) GRIFFIN J A.
PA   (HAFA/) HAFALIA A J A.
PA   (ISON/) ISON C H.
PA   (LALP/) LAL P.
PA   (LEEE/) LEE E A.
PA   (LEES/) LEE S.
PA   (LEES/) LEE S Y.
PA   (MARQ/) MARQUIS J P.
PA   (RAMK/) RAMKUMAR J.
PA   (SPRA/) SPRAGUE W W.
PA   (SWAR/) SWARNAKAR A.
PA   (TANG/) TANG Y T.
PA   (WARR/) WARREN B A.
PA   (YANG/) YANG J.
PA   (YUEH/) YUE H.
PA   (ZEBA/) ZEBARJADIAN Y.
     Query Match   5.1%; Score 112.5; DB 9; Length 807;
     Best Local Similarity   21.8%; Pred. No. 7.2;
RESULT 1087
ID   ABB65440 standard; protein; 1057 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 23112.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.1%; Score 112.5; DB 4; Length 1057;
     Best Local Similarity   21.0%; Pred. No. 11;
RESULT 1088
ID   ABB61305 standard; protein; 1069 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 10707.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.1%; Score 112.5; DB 4; Length 1069;
     Best Local Similarity   21.0%; Pred. No. 11;
RESULT 1089
ID   ABB54963 standard; protein; 1072 AA.
DE   Lactococcus lactis protein yqfG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   5.1%; Score 112.5; DB 5; Length 1072;
     Best Local Similarity   23.3%; Pred. No. 11;
RESULT 1090
ID   ABR58547 standard; protein; 1665 AA.
DE   Human cancer related protein SEQ ID NO:204.
PN   WO2003025138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   5.1%; Score 112.5; DB 6; Length 1665;
     Best Local Similarity   23.8%; Pred. No. 20;
RESULT 1091
ID   ABU56610 standard; protein; 1665 AA.
DE   Lung cancer-associated polypeptide #203.

PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.1%; Score 112.5; DB 6; Length 1665;
Best Local Similarity 23.8%; Pred. No. 20;
RESULT 1092
ID ADN38742 standard; protein; 1665 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:60.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.1%; Score 112.5; DB 7; Length 1665;
Best Local Similarity 23.8%; Pred. No. 20;
RESULT 1093
ID ADN39858 standard; protein; 1666 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C228.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.1%; Score 112.5; DB 7; Length 1666;
Best Local Similarity 23.8%; Pred. No. 20;
RESULT 1094
ID AEF06270 standard; protein; 1773 AA.
DE Human mucin G4.
PN JP2005328749-A.
PD 02-DEC-2005.
PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.
Query Match 5.1%; Score 112.5; DB 10; Length 1773;
Best Local Similarity 26.3%; Pred. No. 22;
RESULT 1095
ID ABB58723 standard; protein; 1844 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2961.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 112.5; DB 4; Length 1844;
Best Local Similarity 24.2%; Pred. No. 23;
RESULT 1096
ID ABB64198 standard; protein; 2406 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19386.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 112.5; DB 4; Length 2406;
Best Local Similarity 20.2%; Pred. No. 34;
RESULT 1097
ID ABP96236 standard; protein; 3065 AA.
DE Human nucleic-acid associated protein 19 SEQ ID NO:19.
PN WO2003016549-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 112.5; DB 6; Length 3065;
Best Local Similarity 23.3%; Pred. No. 48;
RESULT 1098
ID ADQ76693 standard; protein; 298 AA.
DE Human KIM-1 extracellular domain-6xHis fusion.
PN WO2004060041-A2.
PD 22-JUL-2004.
PA (BIOG-) BIOGEN IDEC MA INC.
Query Match 5.1%; Score 112; DB 8; Length 298;
Best Local Similarity 23.3%; Pred. No. 1.9;
RESULT 1099
ID AAM40257 standard; protein; 310 AA.
DE Human polypeptide SEQ ID NO 3402.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 112; DB 4; Length 310;
Best Local Similarity 25.9%; Pred. No. 2;
RESULT 1100
ID AEC32087 standard; protein; 328 AA.
DE Human CG57008-16 protein, SEQ ID NO: 32.
PN US2005197292-A1.

PD 08-SEP-2005.
PA (SMIT/) SMITHSON G.
PA (MESR/) MESRI M.
PA (STAR/) STARLING G.
Query Match 5.1%; Score 112; DB 9; Length 328;
Best Local Similarity 22.3%; Pred. No. 2.2;
RESULT 1101
ID ADJ48582 standard; protein; 363 AA.
DE Oil-associated gene related protein #82.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 5.1%; Score 112; DB 8; Length 363;
Best Local Similarity 25.8%; Pred. No. 2.6;
RESULT 1102
ID AAB11783 standard; protein; 501 AA.
DE Human kinase (PKIN) -17 protein.
PN WO200181555-A2.
PD 01-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 112; DB 4; Length 501;
Best Local Similarity 23.0%; Pred. No. 4;
RESULT 1103
ID AAM38988 standard; protein; 501 AA.
DE Human polypeptide SEQ ID NO 2133.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 112; DB 4; Length 501;
Best Local Similarity 22.3%; Pred. No. 4;
RESULT 1104
ID AAG67539 standard; protein; 501 AA.
DE Amino acid sequence of human kinase 2504.
PN WO200164905-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.1%; Score 112; DB 4; Length 501;
Best Local Similarity 23.0%; Pred. No. 4;
RESULT 1105
ID ADH48722 standard; protein; 501 AA.
DE NOV3 protein sequence, SEQ ID 6.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 112; DB 5; Length 501;
Best Local Similarity 23.0%; Pred. No. 4;
RESULT 1106
ID AEJ61681 standard; protein; 501 AA.
DE Human NOV3 protein, SEQ ID NO: 6.
PN EP1686175-A2.
PD 02-AUG-2006.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 112; DB 5; Length 501;
Best Local Similarity 23.0%; Pred. No. 4;
RESULT 1107
ID ADL14136 standard; protein; 501 AA.
DE Novel human gene 2504 encoded protein.
PN US2004058355-A1.
PD 25-MAR-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.1%; Score 112; DB 8; Length 501;
Best Local Similarity 23.0%; Pred. No. 4;
RESULT 1108
ID ABB67714 standard; protein; 516 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29934.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 112; DB 4; Length 516;

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        Best Local Similarity    22.1%;   Pred. No. 4.2;
RESULT 1109
ID   ADS96468 standard; protein; 516 AA.
DE   Drosophila melanogaster protein, SEQ ID 89.
PN   WO2004039999-A2.
PD   13-MAY-2004.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
     Query Match       5.1%;   Score 112;  DB 8;  Length 516;
     Best Local Similarity    22.1%;   Pred. No. 4.2;
RESULT 1110
ID   AEL96386 standard; protein; 516 AA.
DE   Drosophila melanogaster survival essential protein, SEQ:1278.
PN   US7113558-B1.
PD   14-NOV-2006.
PA   (APPL-) APPLERA CORP.
     Query Match       5.1%;   Score 112;  DB 11;  Length 516;
     Best Local Similarity    22.1%;   Pred. No. 4.2;
RESULT 1111
ID   ADQ76691 standard; protein; 518 AA.
DE   Human KIM-1 extracellular domain-Fc construct.
PN   WO2004060041-A2.
PD   22-JUL-2004.
PA   (BIOG-) BIOGEN IDEC MA INC.
     Query Match       5.1%;   Score 112;  DB 8;  Length 518;
     Best Local Similarity    23.3%;   Pred. No. 4.2;
RESULT 1112
ID   AAB20166 standard; protein; 616 AA.
DE   Mouse protein associated with IgA nephropathy.
PN   WO200105803-A1.
PD   25-JAN-2004.
PA   (GENE-) GENE LOGIC INC.
     Query Match       5.1%;   Score 112;  DB 4;  Length 616;
     Best Local Similarity    21.2%;   Pred. No. 5.4;
RESULT 1113
ID   ADB61539 standard; protein; 656 AA.
DE   Hepatocyte growth factor (HGF) receptor related protein, SEQ ID No 12.
PN   WO200305467-A1.
PD   03-JUL-2003.
PA   (NISB ) JAPAN TOBACCO INC.
     Query Match       5.1%;   Score 112;  DB 7;  Length 656;
     Best Local Similarity    21.2%;   Pred. No. 5.9;
RESULT 1114
ID   ADJ70391 standard; protein; 707 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID2197.
PN   WO200087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
     Query Match       5.1%;   Score 112;  DB 7;  Length 707;
     Best Local Similarity    23.2%;   Pred. No. 6.6;
RESULT 1115
ID   ABU53140 standard; protein; 998 AA.
DE   Human testes-derived protein from DKFZphtes3_2a11.
PN   WO200112659-A2.
PD   22-FEB-2001.
PA   (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match       5.1%;   Score 112;  DB 4;  Length 998;
     Best Local Similarity    21.7%;   Pred. No. 11.
RESULT 1116
ID   ADC31296 standard; protein; 1024 AA.
DE   Human novel polypeptide sequence, SEQ ID NO:1378.
PN   WO2003029271-A2.
PD   10-APR-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match       5.1%;   Score 112;  DB 7;  Length 1024;
     Best Local Similarity    21.7%;   Pred. No. 11.
RESULT 1117
ID   ADZ70351 standard; protein; 1048 AA.
DE   Human protein from lung cancer marker gene FLJ12761.
PN   WO2005032495-A2.
PD   14-APR-2005.
PA   (FARB ) BAYER PHARM CORP.
     Query Match       5.1%;   Score 112;  DB 9;  Length 1048;
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        Best Local Similarity    21.7%;   Pred. No. 12;
RESULT 1118
ID   AD203676 standard; protein.
DE   PRG4-Lub:4 protein.
PN   WO200501130-A2.
PD   24-FEB-2005.
PA   (AMHP ) WYETH.
     Query Match       5.1%;   Score 112;  DB 9;  Length 1069;
     Best Local Similarity    21.7%;   Pred. No. 12;
RESULT 1119
ID   AD280792 standard; protein; 1083 AA.
DE   Amino acid sequence of human homologue of Drosophila gene CG11006.
PN   WO200039635-A2.
PD   06-MAY-2005.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
     Query Match       5.1%;   Score 112;  DB 9;  Length 1083;
     Best Local Similarity    21.7%;   Pred. No. 12;
RESULT 1120
ID   AD203680 standard; protein; 1100 AA.
DE   PRG4-Lub:5 protein.
PN   WO200501130-A2.
PD   24-FEB-2005.
PA   (AMHP ) WYETH.
     Query Match       5.1%;   Score 112;  DB 9;  Length 1100;
     Best Local Similarity    21.7%;   Pred. No. 12;
RESULT 1121
ID   ABG22442 standard; protein; 1180 AA.
DE   Novel human diagnostic protein #22433.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match       5.1%;   Score 112;  DB 4;  Length 1180;
     Best Local Similarity    22.6%;   Pred. No. 14;
RESULT 1122
ID   ABB54070 standard; protein; 1180 AA.
DE   Lactococcus lactis protein yhgD.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match       5.1%;   Score 112;  DB 5;  Length 1180;
     Best Local Similarity    19.9%;   Pred. No. 14;
RESULT 1123
ID   ABB59144 standard; protein; 1348 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 4224.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match       5.1%;   Score 112;  DB 4;  Length 1348;
     Best Local Similarity    20.9%;   Pred. No. 16;
RESULT 1124
ID   ABB60248 standard; protein; 1601 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 7536.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match       5.1%;   Score 112;  DB 4;  Length 1601;
     Best Local Similarity    25.5%;   Pred. No. 21;
RESULT 1125
ID   ABB58595 standard; protein; 4498 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2577.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match       5.1%;   Score 112;  DB 4;  Length 4498;
     Best Local Similarity    25.0%;   Pred. No. 91;
RESULT 1126
ID   ADX91807 standard; protein; 317 AA.
DE   Plant full length insert polypeptide seqid 54471.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
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PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 317;
     Best Local Similarity 38.6%;   Pred. No. 2.3;
RESULT 1127
ID ABU52788 standard; protein; 473 AA.
DE Human signal transduction-associated protein from DKFZphfbr2_82e4.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
     Query Match   5.0%;   Score 111.5;   DB 4;   Length 473;
     Best Local Similarity 38.6%;   Pred. No. 4.1;
RESULT 1128
ID ADU02754 standard; protein; 483 AA.
DE Novel human polypeptide seqid 1221.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 483;
     Best Local Similarity 28.5%;   Pred. No. 4.2;
RESULT 1129
ID AAM93379 standard; protein; 501 AA.
DE Human polypeptide, SEQ ID NO: 2957.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
     Query Match   5.0%;   Score 111.5;   DB 4;   Length 501;
     Best Local Similarity 38.6%;   Pred. No. 4.4;
RESULT 1130
ID ADL30924 standard; protein; 501 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2957.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 501;
     Best Local Similarity 38.6%;   Pred. No. 4.4;
RESULT 1131
ID ABB66957 standard; protein; 514 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27663
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
     Query Match   5.0%;   Score 111.5;   DB 4;   Length 514;
     Best Local Similarity 23.4%;   Pred. No. 4.6;
RESULT 1132
ID ADP07846 standard; protein; 576 AA.
DE Human secreted protein, seq id 329.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 576;
     Best Local Similarity 21.1%;   Pred. No. 5.4;
RESULT 1133
ID ABB11031 standard; peptide; 635 AA.
DE Human secreted protein homologue, SEQ ID NO:1401.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
     Query Match   5.0%;   Score 111.5;   DB 4;   Length 635;
     Best Local Similarity 20.7%;   Pred. No. 6.2;
RESULT 1134
ID ABM83261 standard; protein; 647 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3510.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 647;
     Best Local Similarity 29.9%;   Pred. No. 6.4;
RESULT 1135
ID ADJ96672 standard; protein; 726 AA.
DE Human atypical kinase of the BRD family BRD3 protein SeqID 129.

PN WO2004006838-A2.
PD 22-JAN-2004.
PA (SUGE-) SUGEN INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 726;
     Best Local Similarity 29.9%;   Pred. No. 7.5;
RESULT 1136
ID ADJ54135 standard; protein; 726 AA.
DE Human KIAA0043 polypeptide.
PN US6686147-B1.
PD 03-FEB-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 726;
     Best Local Similarity 29.9%;   Pred. No. 7.5;
RESULT 1137
ID ADP23610 standard; protein; 726 AA.
DE PRO polypeptide SEQ ID NO:788.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 726;
     Best Local Similarity 29.9%;   Pred. No. 7.5;
RESULT 1138
ID ADV97615 standard; protein; 726 AA.
DE Human estrogen receptor binding protein BRD3 Seq 6.
PN JP200500056-A.
PD 06-JAN-2005.
PA (SUMU) SUMITOMO SEIYAKU KK.
     Query Match   5.0%;   Score 111.5;   DB 9;   Length 726;
     Best Local Similarity 29.9%;   Pred. No. 7.5;
RESULT 1139
ID ABB71884 standard; protein; 925 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42444.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
     Query Match   5.0%;   Score 111.5;   DB 4;   Length 925;
     Best Local Similarity 22.2%;   Pred. No. 11;
RESULT 1140
ID ADG14994 standard; protein; 978 AA.
DE Human SECP-27 protein.
PN WO2003087300-A2.
PD 23-OCT-2003.
PA (INCY-) INCYTE CORP.
     Query Match   5.0%;   Score 111.5;   DB 7;   Length 978;
     Best Local Similarity 19.7%;   Pred. No. 11;
RESULT 1141
ID ADR00601 standard; protein; 1072 AA.
DE Human 254P1D6B v.6 protein SEQ ID NO:12.
PN WO2004067716-A2.
PD 12-AUG-2004.
PA (AGEN-) AGENSYS INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 1072;
     Best Local Similarity 19.7%;   Pred. No. 13;
RESULT 1142
ID ADR00597 standard; protein; 1072 AA.
DE Human 254P1D6B v.1 clone LCP-3 protein SEQ ID NO:8.
PN WO2004067716-A2.
PD 12-AUG-2004.
PA (AGEN-) AGENSYS INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 1072;
     Best Local Similarity 19.7%;   Pred. No. 13;
RESULT 1143
ID ADR00598 standard; protein; 1072 AA.
DE Human 254P1D6B v.2 protein SEQ ID NO:9.
PN WO2004067716-A2.
PD 12-AUG-2004.
PA (AGEN-) AGENSYS INC.
     Query Match   5.0%;   Score 111.5;   DB 8;   Length 1072;
     Best Local Similarity 19.7%;   Pred. No. 13;
RESULT 1144
ID ADR00848 standard; protein; 1072 AA.
DE Human 254P1D6B v.1 amino acid sequence SEQ ID NO:259.
PN WO2004067716-A2.

PD   12-AUG-2004.
PA   (AGEN-) AGENSYS INC.
Query Match   5.0%;   Score 111.5; DB 8; Length 1072;
Best Local Similarity 19.7%;   Pred. No. 13;
RESULT 1145
ID   ADR00594 standard; protein; 1072 AA.
DE   Human 254P1D6B v.2 protein SEQ ID NO:5.
PN   WO2004067716-A2.
PD   12-AUG-2004.
PA   (AGEN-) AGENSYS INC.
Query Match   5.0%;   Score 111.5; DB 8; Length 1072;
Best Local Similarity 19.7%;   Pred. No. 13;
RESULT 1146
ID   ABB57882 standard; protein; 1177 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 438.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   5.0%;   Score 111.5; DB 4; Length 1177;
Best Local Similarity 21.2%;   Pred. No. 15;
RESULT 1147
ID   ABB64079 standard; protein; 1186 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 19029.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   5.0%;   Score 111.5; DB 4; Length 1186;
Best Local Similarity 18.2%;   Pred. No. 15;
RESULT 1148
ID   AEK18306 standard; protein; 2194 AA.
DE   Human mucin 4 protein, MUC4.a.
PN   US2006204503-A1.
PD   14-SEP-2006.
PA   (BIOJ) BIOGEN IDEC MA INC.
Query Match   5.0%;   Score 111.5; DB 10; Length 2194;
Best Local Similarity 23.2%;   Pred. No. 36;
RESULT 1149
ID   ABB66878 standard; protein; 2586 AA.
DE   Novel human diagnostic protein #3345.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   5.0%;   Score 111.5; DB 4; Length 2586;
Best Local Similarity 20.4%;   Pred. No. 46;
RESULT 1150
ID   ABG03354 standard; protein; 207 AA.
DE   Novel human diagnostic protein #3345.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   5.0%;   Score 111; DB 4; Length 207;
Best Local Similarity 28.0%;   Pred. No. 1.4;
RESULT 1151
ID   AAU12247 standard; protein; 310 AA.
DE   Human PRO4322 polypeptide.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 4; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1152
ID   AAU09183 standard; protein; 310 AA.
DE   Human PRO4322 polypeptide.
PN   WO200166740-A2.
PD   13-SEP-2001.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 4; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1153
ID   ABB90327 standard; protein; 310 AA.
DE   Human polypeptide SEQ ID NO 2703.
PN   WO200190304-A2.
PD   29-NOV-2001.

PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   5.0%;   Score 111; DB 5; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1154
ID   AAU83705 standard; protein; 310 AA.
DE   Human PRO protein, Seq ID No 228.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 5; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1155
ID   ADY31968 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   WO200193983-A1.
PD   13-DEC-2001.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 5; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1156
ID   ABO17691 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 6; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1157
ID   ABU80852 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 6; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1158
ID   ABO33818 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 6; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1159
ID   ABU80945 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 6; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1160
ID   ABU66645 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 6; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1161
ID   ABU59726 standard; protein; 310 AA.
DE   Novel secreted and transmembrane protein PRO4322.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   5.0%;   Score 111; DB 6; Length 310;
Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1162
ID   ABO24916 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein (PRO) #76.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.

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Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1163
ID  ABU82161 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003008063-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1164
ID  ABU66921 standard; protein; 310 AA.
DE  Human secreted/transmembrane, PRO, protein SEQ ID 152.
PN  US2003032155-A1.
PD  13-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1165
ID  ADA45671 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003022328-A1.
PD  30-JAN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1166
ID  ADA76102 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003073212-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1167
ID  ABJ72341 standard; protein; 310 AA.
DE  Human PRO4322 protein.
PN  US2003050448-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1168
ID  ADA18752 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003054517-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1169
ID  ADA61375 standard; protein; 310 AA.
DE  Homo sapiens.
PN  US2003049816-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1170
ID  ADB19160 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003068796-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1171
ID  ADB27701 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003082704-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1172
ID  ADA86180 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003082711-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1173
ID  ADB15744 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US200308750-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1174
ID  ADA47530 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003073215-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1175
ID  ADA67325 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003068795-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1176
ID  ADB30332 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003068794-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1177
ID  ADA85628 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003082693-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1178
ID  ADA96840 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003082705-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1179
ID  ADA79144 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003082763-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
RESULT 1180
ID  ADA87283 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003087345-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          5.0%;  Score 111; DB 6; Length 310;
Best Local Similarity 25.9%; Pred. No. 2.5;
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RESULT 1181
ID   ADB16485 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1182
ID   ADA91577 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1183
ID   ADB14640 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1184
ID   ADB18601 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1185
ID   ADA93816 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1186
ID   ADB19712 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1187
ID   ADB13024 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1188
ID   ABO43224 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1189
ID   ADA74278 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1190
ID   ADB24511 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1191
ID   ADA82035 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1192
ID   ADA74998 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1193
ID   ADB85076 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1194
ID   ADA84524 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1195
ID   ADB29780 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1196
ID   ADA80308 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1197
ID   ADA75550 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1198
ID   ADA46775 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 6; Length 310;
     Best Local Similarity 25.9%; Pred. No. 2.5;

RESULT 1199
ID   ADB25071 standard; protein; 310 AA.

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DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1200
ID   ADA93247 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1201
ID   ADB26597 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1202
ID   ADB30884 standard; protein; 310 AA.
DE   Human PRO4322 protein.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1203
ID   ABJ72469 standard; protein; 310 AA.
DE   Human PRO4322 protein.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1204
ID   ADA60812 standard; protein; 310 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1205
ID   ADB23959 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH, INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1206
ID   ADA96288 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1207
ID   ADA80860 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1208
ID   ADA95736 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.

PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1209
ID   ADB26045 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1210
ID   ADB21530 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1211
ID   ABO34364 standard; protein; 310 AA.
DE   Human secreted/transmembrane polypeptide PRO 4322.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 6;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1212
ID   ADA77309 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1213
ID   ADB18049 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1214
ID   ADA86732 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1215
ID   ADA87835 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1216
ID   ADA46223 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%; Pred. No. 2.5;
RESULT 1217
ID   ADB28253 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082699-A1.
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PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1218
ID   ADB28805 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1219
ID   ADA76757 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1220
ID   ADA88387 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1221
ID   ADA97392 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1222
ID   ADB27149 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003022239-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1223
ID   ADB22082 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003087344-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1224
ID   ABJ72171 standard; protein; 310 AA.
DE   Human membrane bound receptor/protein PRO4322 amino acid sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1225
ID   ADA66773 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1226
ID   ADB22634 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111;   DB 7;   Length 310;
      Query Match

Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1227
ID   ADB23407 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1228
ID   ADA92129 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1229
ID   ADB15192 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1230
ID   ADB83718 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1231
ID   ADB80824 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1232
ID   ADB73365 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1233
ID   ADB38444 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Query Match

Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1234
ID   ADB78447 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1235
ID   ADB37892 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.   5.0%;   Score 111; DB 7;   Length 310;
      Best Local Similarity   25.9%;   Pred. No. 2.5;

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RESULT 1236
ID   ADB66364 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1237
ID   ADB85095 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1238
ID   ADB89444 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1239
ID   ADB90176 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1240
ID   ADB39277 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1241
ID   ADB78201 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;.  Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1242
ID   ADB87267 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003092890-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1243
ID   ADB84849 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1244
ID   ADB46900 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1245


ID   ADB83964 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1246
ID   ADB86507 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1247
ID   ADB73119 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003109287-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1248
ID   ADB77112 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1249
ID   ADB34269 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1250
ID   ADB35373 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1251
ID   ADB33717 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1252
ID   ADB34821 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1253
ID   ADB35925 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 152.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;   Score 111; DB 7;   Length 310;
     Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1254
ID   ADB46320 standard; protein; 310 AA.
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DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1255
ID   ADC36957 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1256
ID   ADC21947 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1257
ID   ADC50193 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1258
ID   ADC71740 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1259
ID   ADC59719 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1260
ID   ADC49978 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1261
ID   ADC49177 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1262
ID   ADC49694 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1263
ID   ADC47555 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.

PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1264
ID   ADC52726 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID152.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1265
ID   ADC57080 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID152.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1266
ID   ADC60271 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1267
ID   ADC50746 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1268
ID   ADC65273 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1269
ID   ADC54371 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID152.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1270
ID   ADC53332 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID152.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1271
ID   ADC58855 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID152.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             5.0%;  Score 111; DB 7;  Length 310;
     Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1272
ID   ADC55733 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein Seq ID152.
PN   US2003087360-A1.
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PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1273
ID  ADC58303 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein Seq ID152.
PN  US2003087346-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1274
ID  ADC47300 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003105288-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1275
ID  ADD02977 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003092104-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1276
ID  ADC89969 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003087348-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1277
ID  ADC69388 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003194770-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1278
ID  ADC48277 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003194773-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1279
ID  ADD09806 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003194776-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1280
ID  ADC78175 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003096972-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1281
ID  ADD04381 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003087354-A1.
PD  08-MAY-2003.

PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1282
ID  ADD06410 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003073816-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1283
ID  ADC80337 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003092103-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1284
ID  ADD10844 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003194774-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1285
ID  ADC47725 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003194771-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1286
ID  ADC77929 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003088066-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1287
ID  ADC79785 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003087358-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1288
ID  ADD09254 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003105291-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1289
ID  ADD50892 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003105291-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;   Score 111;  DB 7;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1290
ID  ADD40967 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003203438-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
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Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1291
ID   ADD52106 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1292
ID   ADD51138 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1293
ID   ADD52846 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1294
ID   ADD53398 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1295
ID   ADD51554 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1296
ID   ADD02353 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1297
ID   ADD50619 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1298
ID   ADD01787 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1299
ID   ADD53969 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1300
ID   ADD50373 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1301
ID   ADD51384 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1302
ID   ADD92286 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1303
ID   ADD91182 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1304
ID   ADE03796 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1305
ID   ADE32093 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1306
ID   ADE22025 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1307
ID   ADD79249 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1308
ID   ADE41785 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          5.0%;   Score 111; DB 7; Length 310;
Best Local Similarity  25.9%;  Pred. No. 2.5;
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RESULT 1309
ID   ADE17602 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1310
ID   ADD91734 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1311
ID   ADE33197 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1312
ID   ADE33749 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1313
ID   ADD79801 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194768-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1314
ID   ADD92838 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1315
ID   ADE19258 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1316
ID   ADE18706 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1317
ID   ADE42902 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1318

ID   ADD95691 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1319
ID   ADE22577 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1320
ID   ADD78695 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1321
ID   ADE32645 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1322
ID   ADE42337 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1323
ID   ADD80353 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1324
ID   ADD89381 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1325
ID   ADE40665 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1326
ID   ADE04464 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 7; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1327
ID   ADE92593 standard; protein; 310 AA.

DE Human PRO polypeptide #76.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1328
ID ADG21302 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1329
ID ADG22943 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207384-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1330
ID ADF97278 standard; protein; 310 AA.
DE Human PRO polypeptide #76.
PN US2003207370-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1331
ID ADG80342 standard; protein; 310 AA.
DE Human PRO polypeptide #76.
PN US2003207373-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1332
ID ADG79790 standard; protein; 310 AA.
DE Human PRO polypeptide #76.
PN US2003207372-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1333
ID ADH55082 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207381-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1334
ID ADH55634 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207379-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1335
ID ADI63853 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207385-A1.
PD 06-NOV-2003
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1336
ID ADI64802 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.

PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1337
ID ADI63301 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1338
ID ADH81715 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1339
ID ADH81163 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1340
ID ADM82332 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1341
ID ADN15731 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1342
ID ADN16360 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1343
ID ADN15179 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1344
ID ADN14627 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   5.0%;   Score 111; DB 7;   Length 310;
    Best Local Similarity 25.9%;   Pred. No. 2.5;
RESULT 1345
ID ADC49931 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO4322.
PN US2003092888-A1.

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PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1346
ID  ADC80889 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003092115-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1347
ID  ADE21102 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100735-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1348
ID  ADE05946 standard; protein; 310 AA.
DE  Human PRO polypeptide #114.
PN  US2003100728-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1349
ID  ADD76337 standard; protein; 310 AA.
DE  Human PRO polypeptide #114.
PN  US2003100087-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1350
ID  ADD75175 standard; protein; 310 AA.
DE  Human PRO polypeptide #114.
PN  US2003100712-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1351
ID  ADD75921 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100717-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1352
ID  ADD85153 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100722-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1353
ID  ADD86979 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100738-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1354
ID  ADE20856 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100734-A1.
PD  29-MAY-2003.


PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1355
ID  ADE39153 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003096362-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1356
ID  ADD87701 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003092113-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1357
ID  ADD86105 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003203440-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1358
ID  ADE05700 standard; protein; 310 AA.
DE  Human PRO polypeptide #114.
PN  US2003100727-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1359
ID  ADD73685 standard; protein; 310 AA.
DE  Human PRO polypeptide #114.
PN  US2003100711-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1360
ID  ADE75553 standard; protein; 310 AA.
DE  Human PRO polypeptide #114.
PN  US2003211571-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1361
ID  ADD78525 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100737-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1362
ID  ADE23129 standard; protein; 310 AA.
DE  Human PRO polypeptide #76.
PN  US2003092108-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             5.0%;  Score 111;  DB 8;  Length 310;
    Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1363
ID  ADE21348 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO4322.
PN  US2003100736-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
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Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1364
ID   ADD77463 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1365
ID   ADE20610 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1366
ID   ADD75675 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1367
ID   ADD74191 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1368
ID   ADD74437 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1369
ID   ADD76167 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1370
ID   ADD85659 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1371
ID   ADE23681 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1372
ID   ADE24324 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;


Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1373
ID   ADD87149 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1374
ID   ADE05208 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1375
ID   ADD75421 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1376
ID   ADD76965 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1377
ID   ADD86733 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1378
ID   ADE89015 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1379
ID   ADD78201 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1380
ID   ADE18154 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
RESULT 1381
ID   ADE88463 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match              5.0%;   Score 111;  DB 8;  Length 310;
Best Local Similarity   25.9%;   Pred. No. 2.5;
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RESULT 1382
ID   ADD77709 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1383
ID   ADD77955 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1384
ID   ADD85413 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1385
ID   ADD73945 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1386
ID   ADD74683 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1387
ID   ADD77211 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1388
ID   ADD85905 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1389
ID   ADF05454 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1390
ID   ADD74929 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1391

ID   ADE94483 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1392
ID   ADE90894 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1393
ID   ADE95035 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1394
ID   ADE93145 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1395
ID   ADF34726 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1396
ID   ADE92041 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1397
ID   ADE90342 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1398
ID   ADE91489 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1399
ID   ADG05741 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%; Score 111; DB 8; Length 310;
     Best Local Similarity   25.9%; Pred. No. 2.5;
RESULT 1400
ID   ADG27295 standard; protein; 310 AA.

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DE   Human PRO polypeptide #114.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1401
ID   ADG02068 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1402
ID   ADG21854 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1403
ID   ADG19924 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1404
ID   ADF97830 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1405
ID   ADG24047 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1406
ID   ADF98401 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1407
ID   ADG03232 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1408
ID   ADF98953 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1409
ID   ADG16538 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1410
ID   ADG04997 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1411
ID   ADG19264 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1412
ID   ADG11358 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1413
ID   ADG13101 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1414
ID   ADG08158 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1415
ID   ADG15328 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1416
ID   ADG12137 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1417
ID   ADF96726 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.            5.0%;   Score 111;   DB 8;   Length 310;
Query Match
     Best Local Similarity  25.9%;   Pred. No. 2.5;
RESULT 1418
ID   ADG05911 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207374-A1.
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PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1419
ID   ADG23495 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1420
ID   ADG03784 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1421
ID   ADG24685 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1422
ID   ADF94694 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1423
ID   ADG06982 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1424
ID   ADG07534 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1425
ID   ADG06790 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1426
ID   ADG55029 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1427
ID   ADG60693 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207390-A1.
PD   06-NOV-2003.

PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1428
ID   ADG61797 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1429
ID   ADG81998 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1430
ID   ADG57237 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1431
ID   ADG56685 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1432
ID   ADG55581 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1433
ID   ADG58341 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1434
ID   ADG70707 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1435
ID   ADH39134 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      5.0%;      Score 111;   DB 8;   Length 310;
     Best Local Similarity 25.9%;    Pred. No. 2.5;
RESULT 1436
ID   ADG57789 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
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       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1437
ID   ADG53373 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1438
ID   ADG71259 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1439
ID   ADG81446 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1440
ID   ADH30408 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1441
ID   ADH11775 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1442
ID   ADG52197 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1443
ID   ADG53925 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1444
ID   ADG80894 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1445
ID   ADG56113 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1446
ID   ADH12399 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1447
ID   ADG61245 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1448
ID   ADH28332 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1449
ID   ADG54477 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1450
ID   ADG59517 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1451
ID   ADG34224 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1452
ID   ADI80941 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1453
ID   ADI33694 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1454
ID   ADH69788 standard; protein; 310 AA.
DE   Human PRO polypeptide #114.
PN   US2004019183-A1.
PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
       Query Match          5.0%;  Score 111;  DB 8;  Length 310;
       Best Local Similarity  25.9%;  Pred. No. 2.5;
RESULT 1455
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ID   ADG09684 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1456
ID   ADI15155 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1457
ID   ADG09032 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1458
ID   ADI14487 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1459
ID   ADI29949 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1460
ID   ADI18082 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1461
ID   ADM27346 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1462
ID   ADJ63363 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1463
ID   ADJ77258 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1464
ID   ADK66704 standard; protein; 310 AA.

DE   Human PRO polypeptide #114.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1465
ID   ADJ65380 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1466
ID   ADM27516 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1467
ID   ADM42240 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1468
ID   ADM28102 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1469
ID   ADI95584 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1470
ID   ADI96136 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1471
ID   ADS32088 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO4322.
PN   US2004203125-A1.
PD   14-OCT-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1472
ID   ADT03072 standard; protein; 310 AA.
DE   Human PRO polypeptide #76.
PN   US2004214269-A1.
PD   28-OCT-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.0%;
     Best Local Similarity   25.9%; Score 111; DB 8; Length 310;
     Pred. No. 2.5;
RESULT 1473
ID   ADZ03123 standard; protein; 310 AA.
DE   Human secreted/transmembrane PRO4322 protein.

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PN  US2005074837-A1.
PD  07-APR-2005.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 9;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1474
ID  AEB13869 standard; protein; 310 AA.
DE  Cancer cell diagnosis method-related human protein - SEQ ID 152.
PN  US2005153396-A1.
PD  14-JUL-2005.
PA  (BAKE/) BAKER K P.
PA  (BERE/) BERESINI M.
PA  (DEFO/) DEFORGE L.
PA  (DESN/) DESNOYERS L.
PA  (FILV/) FILVAROFF E.
PA  (GAOW/) GAO W.
PA  (GERR/) GERRITSEN M E.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (SHER/) SHERWOOD S.
PA  (SMIT/) SMITH V.
PA  (STEW/) STEWART T A.
PA  (TUMA/) TUMAS D.
PA  (WATA/) WATANABE C K.
PA  (WOOD/) WOOD W I.
PA  (ZHAN/) ZHANG Z.
    Query Match     5.0%;     Score 111; DB 9;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1475
ID  AED86067 standard; protein; 310 AA.
DE  Human PRO amino acid sequence, seq id 152.
PN  US2005245730-A1.
PD  03-NOV-2005.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 9;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1476
ID  AEG21599 standard; protein; 310 AA.
DE  Human protein VYKT1879 (AAQ89137).
PN  WO2006021874-A2.
PD  02-MAR-2006.
PA  (COMP-) COMPUGEN LTD.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1477
ID  AEG21597 standard; protein; 310 AA.
DE  Hypothetical protein Q96DV8/Z40511, version 1.
PN  WO2006021874-A2.
PD  02-MAR-2006.
PA  (COMP-) COMPUGEN LTD.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1478
ID  AEG21596 standard; protein; 310 AA.
DE  Hypothetical protein Q96DV8/Z40511.
PN  WO2006021874-A2.
PD  02-MAR-2006.
PA  (COMP-) COMPUGEN LTD.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.5%;     Pred. No. 2.5; .
RESULT 1479
ID  AEG58014 standard; protein; 310 AA.
DE  Human PRO4322 polypeptide SEQ ID NO: 152.
PN  US2006073568-A1.
PD  06-APR-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1480
ID  AEH49414 standard; protein; 310 AA.
DE  Human secreted polypeptide PRO4322, SEQ ID NO:228.
PN  EP1655177-A2.

PD  24-MAY-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1481
ID  AEI43659 standard; protein; 310 AA.
DE  Human cancer-related PRO protein amino acid sequence - SEQ ID 152.
PN  US200640351-A1.
PD  23-FEB-2006.
PA  (BAKE/) BAKER K P.
PA  (BERE/) BERESINI M.
PA  (DEFO/) DEFORGE L.
PA  (DESN/) DESNOYERS L.
PA  (FILV/) FILVAROFF E.
PA  (GAOW/) GAO W.
PA  (GERR/) GERRITSEN M E.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (SHER/) SHERWOOD S.
PA  (SMIT/) SMITH V.
PA  (STEW/) STEWART T A.
PA  (TUMA/) TUMAS D.
PA  (WATA/) WATANABE C K.
PA  (WOOD/) WOOD W I.
PA  (ZHAN/) ZHANG Z.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1482
ID  AEI23742 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein PRO4322, SEQ ID NO:152.
PN  EP1672070-A2.
PD  21-JUN-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1483
ID  AEK48449 standard; protein; 310 AA.
DE  Human PRO4322 amino acid sequence.
PN  EP1686174-A1.
PD  02-AUG-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1484
ID  AEK63042 standard; protein; 310 AA.
DE  Human PRO4322 polypeptide, SEQ ID NO: 228.
PN  EP1700867-A2.
PD  13-SEP-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1485
ID  AEL17082 standard; protein; 310 AA.
DE  Human secreted polypeptide PRO4322, SEQ ID NO:94.
PN  EP1702928-A2.
PD  20-SEP-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 310;
    Best Local Similarity    25.9%;     Pred. No. 2.5;
RESULT 1486
ID  AEK56676 standard; protein; 455 AA.
DE  Human PRO polypeptide SEQ ID NO:94.
PN  WO2006098887-A2.
PD  21-SEP-2006.
PA  (GETH ) GENENTECH INC.
PA  (LEXI-) LEXICON GENETICS INC.
    Query Match     5.0%;     Score 111; DB 10;  Length 455;
    Best Local Similarity    25.9%;     Pred. No. 4.3;
RESULT 1487
ID  AAM48279 standard; protein; 501 AA.
DE  Human protein kinase.
PN  WO200192492-A2.
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PD 06-DEC-2001.
PA (APPL-) APPLERA CORP.
  Query Match   5.0%;   Score 111; DB 5;   Length 501;
  Best Local Similarity 23.0%;   Pred. No. 4.9;
RESULT 1488
ID AEJ92167 standard; protein; 509 AA.
DE C-terminally truncated Muc1 SEQ ID NO 4.
PN CN1730489-A.
PD 08-FEB-2006.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY MEDICI.
  Query Match   5.0%;   Score 111; DB 10; Length 509;
  Best Local Similarity 28.3%;   Pred. No. 5;
RESULT 1489
ID ABG96378 standard; protein; 515 AA.
DE Human ovarian cancer marker OV45.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match   5.0%;   Score 111; DB 5;   Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1490
ID ADA50565 standard; protein; 515 AA.
DE Human mucin 1 (MUC-1), SEQ ID NO:20.
PN WO200301569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
  Query Match   5.0%;   Score 111; DB 6;   Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1491
ID ABR92123 standard; protein; 515 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:156.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match   5.0%;   Score 111; DB 6;   Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1492
ID AAE37797 standard; protein; 515 AA.
DE Human mucin 1 transmembrane protein.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
  Query Match   5.0%;   Score 111; DB 6;   Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1493
ID ADJ66746 standard; protein; 515 AA.
DE Human Muc1 protein amino acid sequence.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
  Query Match   5.0%;   Score 111; DB 8;   Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1494
ID AEG56872 standard; protein; 515 AA.
DE Human MUC-1 protein, SEQ ID 20.
PN US200606190-A1.
PD 23-MAR-2006.
PA (TRIP-) TRIPATH IMAGING INC.
  Query Match   5.0%;   Score 111; DB 10; Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1495
ID AEJ49785 standard; protein; 515 AA.
DE MUC1 transmembrane protein MUC1/TM.
PN WO2006081553-A2.
PD 03-AUG-2006.
PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
  Query Match   5.0%;   Score 111; DB 10; Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1496
ID AEJ93528 standard; protein; 515 AA.
DE CA15-3 protein.
PN WO2006084387-A1.
PD 17-AUG-2006.

PA (MOUN) MOUNT SINAI HOSPITAL.
PA (IBEX-) IBEX TECHNOLOGIES INC.
  Query Match   5.0%;   Score 111; DB 10; Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1497
ID AEJ92166 standard; protein; 515 AA.
DE Muc1 protein SEQ ID NO 3.
PN CN1730489-A.
PD 08-FEB-2006.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY MEDICI.
  Query Match   5.0%;   Score 111; DB 10; Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1498
ID AEJ92164 standard; protein; 515 AA.
DE Human Muc1 SEQ ID NO 1.
PN CN1730489-A.
PD 08-FEB-2006.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY MEDICI.
  Query Match   5.0%;   Score 111; DB 10; Length 515;
  Best Local Similarity 28.3%;   Pred. No. 5.1;
RESULT 1499
ID ADH10476 standard; protein; 656 AA.
DE Human MUC-1-CPC fusion protein.
PN WO2003104272-A1.
PD 18-DEC-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
PA (GLAX) GLAXO GROUP LTD.
  Query Match   5.0%;   Score 111; DB 8;   Length 656;
  Best Local Similarity 28.3%;   Pred. No. 7.2;
RESULT 1500
ID ABG30261 standard; protein; 661 AA.
DE Novel human diagnostic protein #30252.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match   5.0%;   Score 111; DB 4;   Length 661;
  Best Local Similarity 20.0%;   Pred. No. 7.2;

us-10-677-471-83.rai

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: September 19, 2007, 18:39:54 ; Search time 75 Seconds
                 (without alignments)
                 820.552 Million cell updates/sec

Title: US-10-677-471-83
Perfect score: 2211
Sequence: 1 MFGGGEGSLTYTLVIICFLT.........LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 14278783 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   Issued_Patents_AA:*
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            3: /EMC_Celerra_SIDS2/ptodata/1/iaa/7_COMB.pep:*
            4: /EMC_Celerra_SIDS2/ptodata/1/iaa/H_COMB.pep:*
            5: /EMC_Celerra_SIDS2/ptodata/1/iaa/PCTUS_COMB.pep:*
            6: /EMC_Celerra_SIDS2/ptodata/1/iaa/RE_COMB.pep:*
            7: /EMC_Celerra_SIDS2/ptodata/1/iaa/baCkfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2211	100.0	431	2	US-09-866-028-83	Sequence 83, Appl
2	2211	100.0	431	2	US-09-944-457-83	Sequence 83, Appl
3	2211	100.0	431	2	US-09-945-584-83	Sequence 83, Appl
4	2211	100.0	431	2	US-09-991-181-515	Sequence 515, Appl
5	2211	100.0	431	2	US-09-944-944-83	Sequence 83, Appl
6	2211	100.0	431	2	US-09-990-444-515	Sequence 515, App
7	2211	100.0	431	2	US-09-945-587-83	Sequence 83, Appl
8	2211	100.0	431	2	US-09-997-333-515	Sequence 515, App
9	2211	100.0	431	3	US-09-992-598-515	Sequence 515, App
10	2211	100.0	431	3	US-09-989-735-515	Sequence 515, App
11	2211	100.0	431	3	US-09-989-726-515	Sequence 515, App
12	2211	100.0	431	3	US-09-944-884-83	Sequence 83, Appl
13	2211	100.0	431	3	US-09-997-514-515	Sequence 515, App
14	2211	100.0	431	3	US-09-989-728-515	Sequence 515, App
15	2211	100.0	431	3	US-09-997-349-515	Sequence 515, App
16	2211	100.0	431	3	US-09-997-653-515	Sequence 515, App
17	2211	100.0	431	3	US-09-989-293A-515	Sequence 515, App
18	2211	100.0	431	3	US-09-989-732-515	Sequence 515, App
19	2211	100.0	431	3	US-09-990-441-515	Sequence 515, App
20	2211	100.0	431	3	US-09-989-328-515	Sequence 515, App
21	2211	100.0	431	3	US-09-989-724-515	Sequence 515, App
22	2211	100.0	431	3	US-09-989-733-515	Sequence 515, App
23	2211	100.0	431	3	US-09-993-583-515	Sequence 515, App
24	2211	100.0	431	3	US-09-989-279-515	Sequence 515, App
25	2211	100.0	431	3	US-09-991-157-515	Sequence 515, App
26	2211	100.0	431	3	US-09-990-439-515	Sequence 515, App
27	2211	100.0	431	3	US-09-997-641-515	Sequence 515, App
28	2211	100.0	431	3	US-09-997-384-515	Sequence 515, App
29	2211	100.0	431	3	US-09-989-730-515	Sequence 515, App
30	2211	100.0	431	3	US-09-997-585-515	Sequence 515, App
31	2211	100.0	431	3	US-09-944-896-83	Sequence 83, Appl
32	2211	100.0	431	3	US-09-997-601-515	Sequence 515, App
33	2211	100.0	431	3	US-09-997-666-515	Sequence 515, App
34	188	8.5	449	3	US-10-123-292-224	Sequence 224, App
35	188	8.5	449	3	US-10-152-398-224	Sequence 224, App
36	188	8.5	449	3	US-10-123-907-224	Sequence 224, App
37	188	8.5	449	3	US-10-147-512-224	Sequence 224, App
38	188	8.5	449	3	US-10-147-485-224	Sequence 224, App
39	188	8.5	449	3	US-10-124-814-224	Sequence 224, App
40	188	8.5	449	3	US-10-124-822-224	Sequence 224, App
41	188	8.5	449	3	US-10-131-833A-224	Sequence 224, App
42	188	8.5	449	3	US-10-142-419-224	Sequence 224, App
43	188	8.5	449	3	US-10-152-375-224	Sequence 224, App
44	188	8.5	449	3	US-10-131-818A-224	Sequence 224, App
45	188	8.5	449	3	US-10-145-873-224	Sequence 224, App
46	188	8.5	449	3	US-10-131-822A-224	Sequence 224, App
47	188	8.5	449	3	US-10-128-694A-224	Sequence 224, App
48	188	8.5	449	3	US-10-142-763-224	Sequence 224, App
49	188	8.5	449	3	US-10-128-694A-224	Sequence 224, App
50	188	8.5	449	3	US-10-123-213-224	Sequence 224, App
51	188	8.5	449	3	US-10-123-909-224	Sequence 224, App
52	188	8.5	449	3	US-10-131-826A-224	Sequence 224, App
53	188	8.5	449	3	US-10-147-513-224	Sequence 224, App
54	188	8.5	449	3	US-10-121-043-224	Sequence 224, App
55	188	8.5	449	3	US-10-139-980-224	Sequence 224, App
56	187.5	8.5	417	3	US-10-185-047A-16	Sequence 16, Appl
57	183	8.3	266	2	US-09-489-847-332	Sequence 332, App
58	163	7.4	4262	2	US-10-704-781-4	Sequence 4, Appli
59	163	7.4	4493	2	US-10-704-781-3	Sequence 3, Appli
60	149.5	6.8	5179	2	US-09-538-092-1258	Sequence 1258, Ap
61	145.5	6.6	629	2	US-09-241-581B-6	Sequence 6, Appli
62	145.5	6.6	629	2	US-08-265-428-6	Sequence 6, Appli
63	145.5	6.6	629	5	US-08-765-108-6	Sequence 6, Appli
64	145.5	6.6	629	5	PCT-US95-07721-6	Sequence 6, Appli
65	144.5	6.5	1140	2	US-09-538-092-647	Sequence 647, Appl
66	136	6.2	503	2	US-09-487-558B-424	Sequence 424, App
67	136	6.2	2870	2	US-09-479-467A-15	Sequence 15, Appl
68	136	6.2	2870	2	US-09-655-160-15	Sequence 15, Appl
69	136	6.2	3178	2	US-09-479-467A-4	Sequence 4, Appli
70	136	6.2	3178	2	US-09-655-160-4	Sequence 4, Appli
71	135.5	6.1	2701	3	US-10-171-311-83	Sequence 83, Appl
72	134	6.1	242	3	US-10-703-032-136429	Sequence 136429,
73	133	6.0	556	3	US-09-538-092-712	Sequence 712, App
74	133	6.0	556	2	US-09-487-558B-426	Sequence 426, App
75	133	6.0	1075	2	US-09-487-558B-110	Sequence 110, App
76	132.5	6.0	2283	2	US-10-172-502-4	Sequence 4, Appli
77	132	6.0	788	2	US-09-294-663-3	Sequence 3, Appli
78	132	6.0	807	2	US-09-294-663-4	Sequence 4, Appli
79	132	6.0	1162	2	US-09-745-008-34	Sequence 34, Appl
80	131.5	5.9	5317	2	US-09-668-767-59	Sequence 59, Appl
81	131	5.9	222	3	US-10-703-032-136473	Sequence 136473,
82	129.5	5.9	1367	3	US-09-487-558B-108	Sequence 108, App
83	129	5.8	175	2	US-08-700-651-12	Sequence 12, Appl
84	129	5.8	175	2	US-08-928-361B-17	Sequence 17, Appl
85	129	5.8	175	2	US-09-588-995A-17	Sequence 17, Appl
86	128.5	5.8	634	3	US-10-455-719-235	Sequence 235, App
87	128.5	5.8	634	3	US-10-455-719-360	Sequence 360, App
88	128	5.8	249	2	US-09-745-008-15	Sequence 15, Appl
89	128	5.8	249	2	US-09-588-361B-20	Sequence 20, Appl
90	128	5.8	249	2	US-09-588-995A-20	Sequence 20, Appl
91	128	5.8	605	2	US-09-487-558B-428	Sequence 428, App
92	128	5.8	870	2	US-09-538-092-77	Sequence 77, Appl
93	128	5.8	424	2	US-09-201-228B-421	Sequence 421, App
94	127.5	5.8	577	2	US-09-201-228B-3929	Sequence 3929, Ap
95	127.5	5.8	1601	2	US-09-145-473E-40	Sequence 40, Appl
96	127.5	5.8	1601	2	US-09-862-027-40	Sequence 40, Appl
97	127	5.7	288	3	US-09-216-393B-341	Sequence 341, App
98	127	5.7	288	3	US-09-216-393B-344	Sequence 344, App
99	127	5.7	288	3	US-10-321-856-341	Sequence 341, App

Note: This page is a two-column sequence-listing index printed sideways. The columns have no printed headings; the values are reproduced below in reading order (No. | Score | Score | Length | N | Accession | Sequence). Two rows in the left column (indices 148, 149) could not be resolved in the accession/sequence columns and are left blank.

Left column

No.			Len	N	Accession	Sequence
100	127	5.7	288	3	US-10-321-855-344	Sequence 344, App
101	127	5.7	357	1	US-08-078-683A-8	Sequence 8, Appli
102	127	5.7	357	2	US-08-471-970A-8	Sequence 8, Appli
103	127	5.7	357	2	US-09-723-677B-8	Sequence 8, Appli
104	127	5.7	357	2	US-10-776-989-8	Sequence 8, Appli
105	127	5.7	1322	3	US-09-487-55B-114	Sequence 114, App
106	126.5	5.7	467	2	US-10-455-719-289	Sequence 289, App
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378	111	5.0	2294	US-09-854-856-50	2	Sequence 50, Appl
379	111	5.0	2294	US-10-010-720-50	2	Sequence 50, Appl
380	111	5.0	2322	US-09-854-856-34	2	Sequence 34, Appl
381	111	5.0	2322	US-10-010-720-34	2	Sequence 34, Appl
382	111	5.0	2354	US-09-854-856-18	2	Sequence 18, Appl
383	111	5.0	2354	US-10-010-720-18	2	Sequence 18, Appl
384	111	5.0	2382	US-09-854-856-2	2	Sequence 2, Appli
385	111	5.0	2382	US-10-010-720-2	2	Sequence 2, Appli
386	110	5.0	195	US-09-370-838-125	2	Sequence 125, App
387	110	5.0	195	US-09-854-133-125	2	Sequence 125, App
388	110	5.0	205	US-09-248-796A-21984	2	Sequence 21984, A
389	110	5.0	494	US-07-906-930E-33	1	Sequence 33, Appl
390	110	5.0	517	US-10-455-719-333	3	Sequence 333, App
391	110	5.0	870	US-09-252-691C-6147	3	Sequence 6147, Ap

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392	110	5.0	1404	2	US-10-164-595-78	Sequence 78, Appl
393	110	5.0	1411	2	US-09-949-016-10827	Sequence 10827, A
394	110	5.0	1564	2	US-10-144-198-2	Sequence 2, Appli
395	110	5.0	1564	2	US-10-144-198-4	Sequence 4, Appli
396	110	5.0	3969	2	US-08-061-376-5	Sequence 5, Appli
397	110	5.0	3969	2	US-09-538-092-1262	Sequence 1262, Ap
398	109.5	5.0	124	2	US-08-700-651-11	Sequence 11, Appl
399	109.5	5.0	124	2	US-08-928-361B-16	Sequence 16, Appl
400	109.5	5.0	124	2	US-09-558-995A-16	Sequence 16, Appl
401	109.5	5.0	208	2	US-09-991-181-416	Sequence 416, App
402	109.5	5.0	208	2	US-09-990-444-416	Sequence 416, App
403	109.5	5.0	208	3	US-09-832-129-36	Sequence 36, Appl
404	109.5	5.0	208	3	US-09-997-333-416	Sequence 416, App
405	109.5	5.0	208	3	US-09-992-598-416	Sequence 416, App
406	109.5	5.0	208	3	US-09-989-735-416	Sequence 416, App
407	109.5	5.0	208	3	US-09-989-726-416	Sequence 416, App
408	109.5	5.0	208	3	US-09-997-514-416	Sequence 416, App
409	109.5	5.0	208	3	US-09-988-728-416	Sequence 416, App
410	109.5	5.0	208	3	US-09-997-349-416	Sequence 416, App
411	109.5	5.0	208	3	US-09-997-653-416	Sequence 416, App
412	109.5	5.0	208	3	US-09-988-293A-416	Sequence 416, App
413	109.5	5.0	208	3	US-09-989-732-416	Sequence 416, App
414	109.5	5.0	208	3	US-09-990-441-416	Sequence 416, App
415	109.5	5.0	208	3	US-10-123-292-510	Sequence 510, App
416	109.5	5.0	208	3	US-09-989-328-416	Sequence 416, App
417	109.5	5.0	208	3	US-09-988-724-416	Sequence 416, App
418	109.5	5.0	208	3	US-09-989-733-416	Sequence 416, App
419	109.5	5.0	208	3	US-09-993-583-416	Sequence 416, App
420	109.5	5.0	208	3	US-10-152-398-510	Sequence 510, App
421	109.5	5.0	208	3	US-09-989-279-510	Sequence 510, App
422	109.5	5.0	208	3	US-10-123-907-510	Sequence 510, App
423	109.5	5.0	208	3	US-10-147-512-510	Sequence 510, App
424	109.5	5.0	208	3	US-10-147-485-510	Sequence 510, App
425	109.5	5.0	208	3	US-09-991-157-416	Sequence 416, App
426	109.5	5.0	208	3	US-10-124-814-510	Sequence 510, App
427	109.5	5.0	208	3	US-10-124-822-510	Sequence 510, App
428	109.5	5.0	208	3	US-09-990-439-416	Sequence 416, App
429	109.5	5.0	208	3	US-09-997-641-416	Sequence 416, App
430	109.5	5.0	208	3	US-09-997-384-416	Sequence 416, App
431	109.5	5.0	208	3	US-10-305-278-118	Sequence 118, App
432	109.5	5.0	208	3	US-10-131-833A-510	Sequence 510, App
433	109.5	5.0	208	3	US-10-142-419-510	Sequence 510, App
434	109.5	5.0	208	3	US-09-989-730-416	Sequence 416, App
435	109.5	5.0	208	3	US-10-152-375-510	Sequence 510, App
436	109.5	5.0	208	3	US-09-997-585-416	Sequence 416, App
437	109.5	5.0	208	3	US-10-131-818A-510	Sequence 510, App
438	109.5	5.0	208	3	US-10-145-873-510	Sequence 510, App
439	109.5	5.0	208	3	US-10-152-395-510	Sequence 510, App
440	109.5	5.0	208	3	US-10-131-822A-510	Sequence 510, App
441	109.5	5.0	208	3	US-10-142-763-510	Sequence 510, App
442	109.5	5.0	208	3	US-10-128-694A-510	Sequence 510, App
443	109.5	5.0	364	3	US-10-332-231A-6	Sequence 6, Appl
444	109.5	5.0	389	3	US-10-332-231A-33	Sequence 33, Appl
445	109.5	5.0	389	3	US-10-332-231A-14	Sequence 14, Appl
446	109.5	5.0	483	3	US-09-944-049-14	Sequence 14, Appl
447	109.5	5.0	491	2	US-10-455-719-402	Sequence 402, Appl
448	109.5	5.0	557	2	US-09-248-796A-26892	Sequence 26892, A
449	109.5	5.0	637	1	US-08-847-743B-28	Sequence 28, Appl
450	109.5	5.0	637	1	US-08-456-201-28	Sequence 28, Appl
451	109.5	5.0	637	3	US-08-456-241-28	Sequence 28, Appl
452	109.5	5.0	637	5	US-10-453-183A-5	Sequence 5, Appli
453	109.5	5.0	637	3	PCT-US92-04295A-28	Sequence 28, Appl
454	109.5	5.0	1794	3	US-10-795-159-763	Sequence 763, App
463	109	4.9	413	1	US-08-481-814A-8	Sequence 8, Appli
464	109	4.9	413	2	US-08-836-582-2	Sequence 2, Appli

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465	109	4.9	413	2	US-09-265-566-2	Sequence 2, Appli
466	109	4.9	413	2	US-09-242-737-4	Sequence 4, Appli
467	109	4.9	435	2	US-09-949-016-9671	Sequence 9671, Ap
468	109	4.9	463	2	US-09-345-236B-2	Sequence 2, Appli
469	109	4.9	513	2	US-09-685-558A-18	Sequence 18, Appl
470	109	4.9	513	2	US-09-765-449-18	Sequence 18, Appl
471	109	4.9	529	2	US-09-742-201-2	Sequence 2, Appli
472	109	4.9	529	3	US-10-223-081-42	Sequence 42, Appl
473	109	4.9	529	3	US-10-223-087-42	Sequence 42, Appl
474	109	4.9	529	3	US-10-223-082-42	Sequence 42, Appl
475	109	4.9	529	3	US-10-223-084-42	Sequence 42, Appl
476	109	4.9	529	3	US-10-245-913-10	Sequence 10, Appl
477	109	4.9	529	3	US-10-245-752-10	Sequence 10, Appl
478	109	4.9	529	3	US-10-242-095-10	Sequence 10, Appl
479	109	4.9	529	3	US-10-242-652-10	Sequence 10, Appl
480	109	4.9	529	3	US-10-223-090-42	Sequence 42, Appl
481	109	4.9	567	3	US-10-455-719-227	Sequence 227, App
482	109	4.9	569	2	US-09-248-796A-16697	Sequence 16697, A
483	109	4.9	571	2	US-09-949-016-10184	Sequence 10184, A
484	109	4.9	575	3	US-10-123-292-128	Sequence 128, App
485	109	4.9	575	3	US-10-152-398-128	Sequence 128, App
486	109	4.9	575	3	US-10-123-907-128	Sequence 128, App
487	109	4.9	575	3	US-10-147-512-128	Sequence 128, App
488	109	4.9	575	3	US-10-147-485-128	Sequence 128, App
489	109	4.9	575	3	US-10-124-814-128	Sequence 128, App
490	109	4.9	575	3	US-10-124-822-128	Sequence 128, App
491	109	4.9	575	3	US-10-131-833A-128	Sequence 128, App
492	109	4.9	575	3	US-10-142-419-128	Sequence 128, App
493	109	4.9	575	3	US-10-152-375-128	Sequence 128, App
494	109	4.9	575	3	US-10-131-818A-128	Sequence 128, App
495	109	4.9	575	3	US-10-145-873-128	Sequence 128, App
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505	109	4.9	575	3	US-10-139-980-128	Sequence 128, App
506	109	4.9	612	2	US-08-467-602-228	Sequence 228, App
507	109	4.9	612	3	US-08-411-295F-154	Sequence 154, App
508	109	4.9	612	3	US-08-461-097-228	Sequence 228, App
509	109	4.9	612	3	US-08-209-204E-228	Sequence 228, App
510	109	4.9	646	2	US-08-467-602-270	Sequence 270, App
511	109	4.9	646	3	US-08-411-295F-196	Sequence 196, App
512	109	4.9	646	3	US-08-461-097-270	Sequence 270, App
513	109	4.9	646	3	US-08-209-204E-270	Sequence 270, App
514	109	4.9	668	1	US-07-891-942G-6	Sequence 6, Appli
515	109	4.9	707	3	US-10-195-144-31	Sequence 31, Appl
516	109	4.9	861	3	US-10-470-335-251	Sequence 251, App
517	109	4.9	861	3	US-08-467-602-312	Sequence 312, App
518	109	4.9	861	3	US-08-411-295F-238	Sequence 238, App
519	109	4.9	861	3	US-08-461-097-312	Sequence 312, App
520	109	4.9	861	3	US-08-209-204E-312	Sequence 312, App
521	109	4.9	895	2	US-08-467-602-354	Sequence 354, App
522	109	4.9	895	3	US-08-411-295F-280	Sequence 280, App
523	109	4.9	895	3	US-08-461-097-354	Sequence 354, App
524	109	4.9	895	3	US-08-209-204E-354	Sequence 354, App
525	109	4.9	925	3	US-10-108-260A-3889	Sequence 3889, Ap
526	109	4.9	937	3	US-10-455-719-236	Sequence 236, App
527	109	4.9	937	3	US-10-455-719-326	Sequence 326, App
528	108.5	4.9	362	2	US-09-248-796A-21767	Sequence 21767, A
529	108.5	4.9	382	2	US-09-248-796A-17276	Sequence 17276, A
530	108.5	4.9	603	2	US-08-467-602-216	Sequence 216, App
531	108.5	4.9	603	3	US-08-411-295F-142	Sequence 142, App
532	108.5	4.9	603	3	US-08-461-097-216	Sequence 216, App
533	108.5	4.9	603	3	US-08-209-204E-216	Sequence 216, App
534	108.5	4.9	637	2	US-08-467-602-258	Sequence 258, App
535	108.5	4.9	637	3	US-08-411-295F-184	Sequence 184, App
536	108.5	4.9	637	3	US-08-461-097-258	Sequence 258, App
537	108.5	4.9	637	3	US-08-209-204E-258	Sequence 258, App

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539	108.5	4.9	747	2	US-09-949-016-10268	Sequence 10268, A
540	108.5	4.9	852	2	US-08-470-335-248	Sequence 248, App
541	108.5	4.9	852	2	US-08-467-602-300	Sequence 300, App
542	108.5	4.9	852	2	US-08-411-295F-226	Sequence 226, App
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544	108.5	4.9	852	3	US-08-209-204E-300	Sequence 300, App
545	108.5	4.9	886	2	US-08-467-602-342	Sequence 342, App
546	108.5	4.9	886	2	US-08-411-295F-268	Sequence 268, App
547	108.5	4.9	886	2	US-08-461-097-342	Sequence 342, App
548	108.5	4.9	886	2	US-08-209-204E-342	Sequence 342, A
549	108	4.9	298	2	US-09-248-796A-26762	Sequence 26762, A
550	108	4.9	460	2	US-09-949-016-8029	Sequence 8029, Ap
551	108	4.9	581	3	US-10-225-066A-272	Sequence 272, App
552	108	4.9	661	3	US-08-417-174-27	Sequence 27, Appl
553	108	4.9	661	1	US-08-417-174-121	Sequence 121, App
554	108	4.9	661	1	US-08-231-565A-27	Sequence 27, Appl
555	108	4.9	661	1	US-09-007-961-27	Sequence 27, Appl
556	108	4.9	661	2	US-09-267-439-27	Sequence 27, Appl
557	108	4.9	661	2	US-09-267-439-121	Sequence 121, App
558	108	4.9	661	2	US-08-388-852B-2	Sequence 2, Appli
559	108	4.9	661	2	US-09-073-138-27	Sequence 27, Appl
560	108	4.9	661	2	US-09-073-138-121	Sequence 121, App
561	108	4.9	661	2	US-09-862-260A-2	Sequence 2, Appli
562	108	4.9	661	2	US-09-898-860-27	Sequence 27, Appl
563	108	4.9	661	3	US-09-898-860-121	Sequence 121, App
564	108	4.9	661	3	US-10-685-977-27	Sequence 27, Appl
565	108	4.9	661	3	US-10-685-977-121	Sequence 121, App
566	108	4.9	703	2	US-08-910-925-4	Sequence 4, Appli
567	108	4.9	717	2	US-08-910-925-1	Sequence 1, Appli
568	108	4.9	983	2	US-09-538-092-1320	Sequence 1320, Ap
569	108	4.9	1481	1	US-08-616-844-40	Sequence 40, Appl
570	108	4.9	1481	1	US-08-599-654-40	Sequence 40, Appl
571	108	4.9	1481	2	US-08-944-868A-40	Sequence 40, Appl
572	108	4.9	1481	2	US-08-944-423A-40	Sequence 40, Appl
573	108	4.9	1481	2	US-08-944-496-40	Sequence 40, Appl
574	107.5	4.9	453	2	US-09-686-583B-12	Sequence 12, Appl
575	107.5	4.9	453	2	US-10-401-324A-12	Sequence 12, Appl
576	107.5	4.9	475	1	US-08-861-464-14	Sequence 14, Appl
577	107.5	4.9	475	1	US-08-396-001-14	Sequence 14, Appl
578	107.5	4.9	475	2	US-09-323-433A-14	Sequence 14, Appl
579	107.5	4.9	475	2	US-09-826-752-14	Sequence 14, Appl
580	107.5	4.9	596	2	US-10-012-231A-243	Sequence 243, App
581	107.5	4.9	596	2	US-10-015-389A-243	Sequence 243, App
582	107.5	4.9	596	2	US-10-006-768A-243	Sequence 243, App
583	107.5	4.9	596	2	US-10-015-671A-243	Sequence 243, App
584	107.5	4.9	596	2	US-10-015-393A-243	Sequence 243, App
585	107.5	4.9	596	2	US-10-011-833A-243	Sequence 243, App
586	107.5	4.9	596	2	US-10-006-041A-243	Sequence 243, App
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589	107.5	4.9	596	2	US-10-011-795B-243	Sequence 243, App
590	107.5	4.9	596	3	US-10-015-386A-243	Sequence 243, App
591	107.5	4.9	596	3	US-10-012-121A-243	Sequence 243, App
592	107.5	4.9	596	3	US-10-006-485A-243	Sequence 243, App
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594	107.5	4.9	596	3	US-10-012-752A-243	Sequence 243, App
595	107.5	4.9	596	3	US-10-017-253A-243	Sequence 243, App
596	107.5	4.9	596	3	US-10-015-519A-243	Sequence 243, App
597	107.5	4.9	596	3	US-10-007-236A-243	Sequence 243, App
598	107.5	4.9	596	3	US-10-012-149A-243	Sequence 243, App
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604	107.5	4.9	596	3	US-10-006-172A-243	Sequence 243, App
605	107.5	4.9	596	3	US-10-063-639A-100	Sequence 100, App
606	107.5	4.9	596	3	US-10-015-395A-243	Sequence 243, App
607	107.5	4.9	596	3	US-10-183-001-310	Sequence 310, App
608	107.5	4.9	596	3	US-10-015-610A-243	Sequence 243, App
609	107.5	4.9	596	3	US-10-180-998-310	Sequence 310, App
610	107.5	4.9	596	3	US-10-201-769-310	Sequence 310, App
611	107.5	4.9	596	3	US-10-006-130A-243	Sequence 243, App
612	107.5	4.9	596	3	US-10-063-638A-100	Sequence 100, App
613	107.5	4.9	596	3	US-10-063-510-100	Sequence 100, App
614	107.5	4.9	596	3	US-10-063-741-100	Sequence 100, App
615	107.5	4.9	596	3	US-10-063-584-100	Sequence 100, App
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617	107.5	4.9	596	3	US-10-174-581-310	Sequence 310, App
618	107.5	4.9	596	3	US-10-006-867-310	Sequence 310, App
619	107.5	4.9	596	3	US-10-063-659-100	Sequence 100, App
620	107.5	4.9	596	2	US-10-015-869A-243	Sequence 243, App
621	107.5	4.9	596	3	US-10-063-742-100	Sequence 100, App
622	107.5	4.9	596	2	US-10-063-703-100	Sequence 100, App
623	107.5	4.9	596	3	US-10-063-709-100	Sequence 100, App
624	107.5	4.9	596	3	US-10-063-581-100	Sequence 100, App
625	107.5	4.9	596	3	US-10-063-593-100	Sequence 100, App
626	107.5	4.9	596	3	US-10-063-599-100	Sequence 100, App
627	107.5	4.9	596	3	US-10-063-646-100	Sequence 100, App
628	107.5	4.9	596	3	US-10-063-660-100	Sequence 100, App
629	107.5	4.9	596	3	US-10-207-916-310	Sequence 310, App
630	107.5	4.9	596	3	US-10-063-647-100	Sequence 100, App
631	107.5	4.9	596	3	US-10-063-661-100	Sequence 100, App
632	107.5	4.9	596	3	US-10-063-651-100	Sequence 100, App
633	107.5	4.9	596	3	US-10-063-530-100	Sequence 100, App
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635	107.5	4.9	596	3	US-10-063-648-100	Sequence 100, App
636	107.5	4.9	596	3	US-10-063-657-100	Sequence 100, App
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638	107.5	4.9	596	3	US-10-063-529-100	Sequence 100, App
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640	107.5	4.9	596	3	US-10-063-585-100	Sequence 100, App
641	107.5	4.9	596	3	US-10-063-591A-100	Sequence 100, App
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643	107.5	4.9	596	3	US-10-063-532-100	Sequence 100, App
644	107.5	4.9	596	3	US-10-063-654-100	Sequence 100, App
645	107.5	4.9	596	3	US-10-063-582-100	Sequence 100, App
646	107.5	4.9	596	3	US-10-063-524-100	Sequence 100, App
647	107.5	4.9	596	3	US-10-972-317-100	Sequence 100, App
648	107.5	4.9	596	3	US-10-174-583-310	Sequence 310, App
649	107.5	4.9	596	3	US-10-063-551-100	Sequence 100, App
650	107.5	4.9	596	3	US-10-063-650-100	Sequence 100, App
651	107.5	4.9	596	3	US-10-063-523-100	Sequence 100, App
652	107.5	4.9	596	3	US-10-063-592A-100	Sequence 100, App
653	107.5	4.9	596	3	US-10-063-705-100	Sequence 100, App
654	107.5	4.9	596	3	US-10-063-598-100	Sequence 100, App
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672	107.5	4.9	693	2	US-09-752-639-154	Sequence 154, App
673	107.5	4.9	693	2	US-09-712-813-154	Sequence 154, App
674	107.5	4.9	693	2	US-09-700-354A-154	Sequence 154, App
675	107.5	4.9	713	2	US-09-487-558B-408	Sequence 408, App
676	107.5	4.9	1225	2	US-09-501-171-4	Sequence 4, Appli
677	107.5	4.9	1225	2	US-09-949-016-6063	Sequence 6063, Ap
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679	107.5	4.9	1461	2	US-10-094-749-2733	Sequence 2733, Ap
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681	107.5	4.9	2414	5	US-09-538-092-1289	Sequence 1289, Ap
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692	106.5	4.8	545	2	US-10-775-649-4	Sequence 4, Appli
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695	106.5	4.8	713	2	US-08-477-346-63	Sequence 63, Appl
696	106.5	4.8	713	2	US-08-473-089-63	Sequence 63, Appl
697	106.5	4.8	713	2	US-08-487-072A-63	Sequence 63, Appl
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772	104.5	4.7	626	3	US-08-461-097-222	Sequence 222, App
773	104.5	4.7	626	2	US-08-209-204E-222	Sequence 222, App
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804	104.5	4.7	875	2	US-08-461-097-306	Sequence 306, App
805	104.5	4.7	875	3	US-08-461-097-369	Sequence 369, App
806	104.5	4.7	875	2	US-08-209-204E-306	Sequence 306, App
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843	103	4.7	578	3	US-08-209-204E-249	Sequence 249, App
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917	102.5	4.6	603	2	US-08-209-204E-235	Sequence 235, App
918	102.5	4.6	603	2	US-08-467-602-279	Sequence 279, App
919	102.5	4.6	603	3	US-08-411-295F-205	Sequence 205, App
920	102.5	4.6	603	3	US-08-461-097-279	Sequence 279, App
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922	102.5	4.6	606	2	US-08-467-602-214	Sequence 214, App
923	102.5	4.6	606	2	US-08-467-602-277	Sequence 277, App
924	102.5	4.6	606	3	US-08-411-295F-140	Sequence 140, App
925	102.5	4.6	606	3	US-08-411-295F-203	Sequence 203, App
926	102.5	4.6	606	3	US-08-461-097-214	Sequence 214, App
927	102.5	4.6	606	3	US-08-461-097-277	Sequence 277, App
928	102.5	4.6	606	3	US-08-209-204E-214	Sequence 214, App
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934	102.5	4.6	640	3	US-08-411-295F-182	Sequence 182, App
935	102.5	4.6	640	3	US-08-461-097-256	Sequence 256, App
936	102.5	4.6	640	3	US-08-209-204E-256	Sequence 256, App
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948	102.5	4.6	669	5	US-10-453-183A-1	Sequence 1, Appli
949	102.5	4.6	669	5	PCT-US92-04295A-8	Sequence 8, Appli
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957	102.5	4.6	818	2	US-08-470-335-234	Sequence 234, App
958	102.5	4.6	818	2	US-08-467-602-321	Sequence 321, App
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961	102.5	4.6	818	3	US-08-209-204E-321	Sequence 321, App
962	102.5	4.6	821	2	US-08-470-335-228	Sequence 228, App
963	102.5	4.6	821	2	US-08-467-602-319	Sequence 319, App
964	102.5	4.6	821	3	US-08-411-295F-245	Sequence 245, App
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968	102.5	4.6	852	2	US-08-411-295F-289	Sequence 289, App
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981	102.5	4.6	889	3	US-08-411-295F-266	Sequence 266, App
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1046	101.5	4.6	450	3	US-08-209-204E-195	Sequence 195, App
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1074	101.5	4.6	635	2	US-08-411-295F-220	Sequence 220, App
1075	101.5	4.6	635	3	US-08-461-097-231	Sequence 231, App
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1077	101.5	4.6	635	3	US-08-209-204E-231	Sequence 231, App
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1081	101.5	4.6	649	3	US-08-209-204E-267	Sequence 267, App
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1085	101.5	4.6	669	3	US-08-461-097-273	Sequence 273, App
1086	101.5	4.6	669	2	US-08-209-204E-273	Sequence 273, App
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1094	101.5	4.6	830	3	US-08-209-204E-330	Sequence 330, App
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1097	101.5	4.6	850	3	US-08-461-097-336	Sequence 336, App
1098	101.5	4.6	850	3	US-08-209-204E-336	Sequence 336, App
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1117	101.5	4.6	884	3	US-08-209-204E-315	Sequence 315, App
1118	101.5	4.6	884	3	US-08-209-204E-378	Sequence 378, App
1119	101.5	4.6	898	3	US-08-467-602-351	Sequence 351, App
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1126	918	3	101.5	4.6	US-08-209-204E-357	Sequence 357, App
1127	1443	3	101.5	4.6	US-10-455-719-217	Sequence 217, App
1128	3892	2	101.5	4.6	US-09-328-352-5503	Sequence 5503, Ap
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1194	782	2	100	4.5	US-09-684-708A-21	Sequence 21, Appl

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382	95	4.3	382	US-10-423-649-2	Sequence 2, Appli
446	95	4.3	446	US-08-922-171-3	Sequence 3, Appli
472	95	4.3	472	US-08-922-171-2	Sequence 2, Appli
748	95	4.3	748	US-10-108-260A-3747	Sequence 3747, Ap
855	95	4.3	855	US-08-816-693A-2	Sequence 2, Appli
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855	95	4.3	855	US-09-496-672-2	Sequence 2, Appli
903	95	4.3	903	US-09-618-425-11	Sequence 11, Appl
903	95	4.3	903	US-08-853-310-2	Sequence 2, Appli
903	95	4.3	903	US-09-193-562D-46	Sequence 46, Appl
903	95	4.3	903	US-09-623-624-18	Sequence 18, Appl
903	95	4.3	903	US-10-055-412B-46	Sequence 46, Appl
903	95	4.3	903	US-10-270-595-18	Sequence 18, Appl
927	95	4.3	927	US-10-772-437-18	Sequence 18, Appl
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1438	95	4.3	1438	US-09-206-942-43	Sequence 43, Appl
1651	95	4.3	1651	US-09-538-092-189	Sequence 189, App
1651	95	4.3	1651	US-10-289-776-18	Sequence 18, Appl
1651	95	4.3	1651	US-09-191-665-18	Sequence 8, Appli
2186	95	4.3	2186	US-09-949-016-10828	Sequence 10828, A
2349	95	4.3	2349	US-09-538-092-914	Sequence 914, App
2349	95	4.3	2349	US-09-762-577B-68	Sequence 68, Appl
2385	95	4.3	2385	US-09-543-681A-6304	Sequence 6304, Ap
165	94.5	4.3	165	US-09-248-796A-23180	Sequence 23180, A
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281	94.5	4.3	281	US-10-703-032-113164	Sequence 113164,
332	94.5	4.3	332	US-08-818-112-53	Sequence 53, Appl
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332	94.5	4.3	332	US-10-886-349A-41	Sequence 41, Appl
332	94.5	4.3	332	US-11-082-005-53	Sequence 53, Appl
332	94.5	4.3	332	US-11-028-898-53	Sequence 53, Appl
335	94.5	4.3	335	US-09-107-43-3853	Sequence 3853, Ap
342	94.5	4.3	342	US-09-605-703B-250	Sequence 250, App
380	94.5	4.3	380	US-09-270-767-43987	Sequence 43987, A
404	94.5	4.3	404	US-09-252-691C-8162	Sequence 8162, Ap
449	94.5	4.3	449	US-10-163-774-3	Sequence 3, Appl
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502	94.5	4.3	502	US-09-960-022-10	Sequence 10, Appl
566	94.5	4.3	566	US-09-538-092-724	Sequence 724, Appl
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1057	94.5	4.3	1057	US-10-108-260A-3230	Sequence 3230, Ap
1060	94.5	4.3	1060	US-08-911-393-2	Sequence 2, Appli
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1487	94.5	4.3	1702	US-08-296-791-5	Sequence 5, Appli
1488	94.5	4.3	1702	US-09-839-996-5	Sequence 5, Appli
1489	94.5	4.3	1702	US-10-080-505-5	Sequence 5, Appli
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1491	94.5	4.3	1702	US-10-687-046-5	Sequence 5, Appli
1492	94.5	4.3	1702	PCT-US95-10661A-5	Sequence 5, Appli
1493	94	4.3	154	US-10-703-032-120174	Sequence 120174,
1494	94	4.3	330	US-10-703-032-120376	Sequence 120376,
1495	94	4.3	539	US-09-252-991A-33061	Sequence 33061, A
1496	94	4.3	631	US-08-605-541B-12	Sequence 12, Appl
1497	94	4.3	631	US-09-902-540-12106	Sequence 12106, A
1498	94	4.3	644	US-09-619-049-1362	Sequence 1362, Ap
1499	94	4.3	645	US-09-964-899-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
US-09-866-028-83
; Sequence 83, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Godard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-83

Query Match   100.0%; Score 2211; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.4e-201;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-944-457-83
; Sequence 83, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin
;   APPLICANT: Botstein, David
;   APPLICANT: Eaton, Dan
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Gerritsen, Mary
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul
;   APPLICANT: Grimaldi, Christopher
;   APPLICANT: Gurney, Austin
;   APPLICANT: Hillan, Kenneth
;   APPLICANT: Kljavin, Ivar
;   APPLICANT: Napier, Mary
;   APPLICANT: Roy, Margaret
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Wood, William
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P2548P1C1
;   CURRENT APPLICATION NUMBER: US/09/944,457
;   CURRENT FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: 09/866,028
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: 60/067,411
;   PRIOR FILING DATE: December 3, 1997
;   PRIOR APPLICATION NUMBER: 60/069,334
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069335
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,278
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,425
;   PRIOR FILING DATE: December 12, 1997
;   PRIOR APPLICATION NUMBER: 60/069,696
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,694
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,702
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,870
;   PRIOR FILING DATE: December 17, 1997
;   PRIOR APPLICATION NUMBER: 60/069,873
;   PRIOR FILING DATE: December 17, 1997
;   PRIOR APPLICATION NUMBER: 60/068,017
;   PRIOR FILING DATE: December 18, 1997
;   PRIOR APPLICATION NUMBER: 60/070,440
;   PRIOR FILING DATE: January 5, 1998
;   PRIOR APPLICATION NUMBER: 60/074,086
;   PRIOR FILING DATE: February 9, 1998
;   PRIOR APPLICATION NUMBER: 60/074,092
;   PRIOR FILING DATE: February 9, 1998
;   PRIOR APPLICATION NUMBER: 60/075,945
;   PRIOR FILING DATE: February 25, 1998
;   PRIOR APPLICATION NUMBER: 60/112,850
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 60/113,296
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 60/146,222
;   PRIOR FILING DATE: July 28, 1999
;   PRIOR APPLICATION NUMBER: PCT/US98/19330
;   PRIOR FILING DATE: September 16, 1998
;   PRIOR APPLICATION NUMBER: PCT/US98/25108
;   PRIOR FILING DATE: December 1, 1998
;   PRIOR APPLICATION NUMBER: 09/216,021
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 09/218,517
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 09/254,311
;   PRIOR FILING DATE: March 3, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/12252
;   PRIOR FILING DATE: June 22, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/21090
;   PRIOR FILING DATE: September 15, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28409
;   PRIOR FILING DATE: No. 6734288ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28313
;   PRIOR FILING DATE: No. 6734288ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28301
;   PRIOR FILING DATE: December1, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/30095
;   PRIOR FILING DATE: December 16, 1999
;   PRIOR APPLICATION NUMBER: PCT/US00/03565
;   PRIOR FILING DATE: February 11, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/04414
;   PRIOR FILING DATE: February 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/05841
;   PRIOR FILING DATE: March 2, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/08439
;   PRIOR FILING DATE: March 30, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/14042
;   PRIOR FILING DATE: May 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/20710
;   PRIOR FILING DATE: July 28, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/32678
;   PRIOR FILING DATE: December 1, 2000
;   PRIOR APPLICATION NUMBER: PCT/US01/06520
;   PRIOR FILING DATE: February 28, 2001
;   NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
;   LENGTH: 431
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-457-83

Query Match   100.0%; Score 2211; DB 2; Length 431;
Best Local Similarity   100.0%; Pred. No. 1.4e-201;
Matches   431; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
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Qy   361  EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420
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RESULT 3
US-09-945-584-83

; Sequence 83, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
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; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 83
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-584-83

Query Match   100.0%; Score 2211; DB 2; Length 431;
Best Local Similarity   100.0%; Pred. No. 1.4e-201;
Matches 431; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
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Qy    61  EDCINSCCSTRNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120
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Qy   181  HLEKLFKMDEASAQLLAYKEKGHSQSSDQEIAHLLPENVSALPATVAVASPHTTSA  240
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Qy   301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR   360
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Db   301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR   360

Qy   361  EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRIILSESLRRKRYSRL  420
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Db   361  EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRIILSESLRRKRYSRL  420

Qy   421  DYLINGIYVDI  431
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Db   421  DYLINGIYVDI  431
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RESULT 4
US-09-991-181-515
; Sequence 515, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-02

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Query Match          100.0%;  Score 2211;  DB 2;  Length 431;
Best Local Similarity 100.0%;  Pred. No. 1.4e-201;
Matches  431;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy     61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Db     61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

Qy    121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180
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Db    121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy    181 HLEKLFKMDEASAQLLAYKEKGHSQSQSFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db    181 HLEKLFKMDEASAQLLAYKEKGHSQSQSFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy    241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAAATLQAMATT 300
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Db    241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAAATLQAMATT 300

Qy    301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Qy    421 DYLINGIYVDI 431
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RESULT 5
US-09-944-944-83
; Sequence 83, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
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; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: 1998-07-09
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18

Query Match　　　　100.0%;　　Score 2211;　DB 2;　　Length 431;
Best Local Similarity　100.0%;　Pred. No. 1.4e-201;
Matches 431;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Db    1  MFFGGEGSLYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ   60

Qy   61  EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120
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Db   61  EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120

Qy  121  TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD  180
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Db  121  TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD  180

Qy  181  HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA  240
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Db  181  HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA  240

Qy  241  TPKPATLLPTNASVTPSGTSQPQLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT  300
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Db  241  TPKPATLLPTNASVTPSGTSQPQLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT  300

Qy  301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR  360

Qy  361  EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420

Qy  421  DYLINGIYVDI  431
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Db  421  DYLINGIYVDI  431
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RESULT 6
US-09-990-444-515
; Sequence 515, Application US/09990444
Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120

SEQ ID NO 83
LENGTH: 431
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-944-83

PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; ,, PRIOR APPLICATION NUMBER: 60/091626
; ,, PRIOR FILING DATE: 1998-07-02
; ,, PRIOR APPLICATION NUMBER: 60/091633
; ,, PRIOR FILING DATE: 1998-07-02
; ,, PRIOR APPLICATION NUMBER: 60/091978
; ,, PRIOR FILING DATE: 1998-07-07
; ,, PRIOR APPLICATION NUMBER: 60/091982
; ,, PRIOR FILING DATE: 1998-07-07
; ,, PRIOR APPLICATION NUMBER: 60/092182
; ,, PRIOR FILING DATE: 1998-07-09

; ,, APPLICANT: Gurney,Austin
; ,, APPLICANT: Hillan,Kenneth
; ,, APPLICANT: Kljavin,Ivar
; ,, APPLICANT: Napier,Mary
; ,, APPLICANT: Roy,Margaret
; ,, APPLICANT: Tumas,Daniel
; ,, APPLICANT: Wood,William
; ,, TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ,, TITLE OF INVENTION: ACIDS ENCODING THE SAME
; ,, FILE REFERENCE: P2548P1C1
; ,, CURRENT APPLICATION NUMBER: US/09/945,587
; ,, CURRENT FILING DATE: 2001-09-26
; ,, PRIOR APPLICATION NUMBER: 09/866,028
; ,, PRIOR FILING DATE: 2001-05-25
; ,, PRIOR APPLICATION NUMBER: 60/067,411
; ,, PRIOR FILING DATE: December 3, 1997
; ,, PRIOR APPLICATION NUMBER: 60/069,334
; ,, PRIOR FILING DATE: December 11, 1997
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; ,, PRIOR APPLICATION NUMBER: 60/069,425
; ,, PRIOR FILING DATE: December 12, 1997
; ,, PRIOR APPLICATION NUMBER: 60/069,696
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; ,, PRIOR FILING DATE: December 18, 1997
; ,, PRIOR APPLICATION NUMBER: 60/070,440
; ,, PRIOR FILING DATE: January 5, 1998
; ,, PRIOR APPLICATION NUMBER: 60/074,086
; ,, PRIOR FILING DATE: February 9, 1998
; ,, PRIOR APPLICATION NUMBER: 60/074,092
; ,, PRIOR FILING DATE: February 9, 1998
; ,, PRIOR APPLICATION NUMBER: 60/075,945
; ,, PRIOR FILING DATE: February 25, 1998
; ,, PRIOR APPLICATION NUMBER: 60/112,850
; ,, PRIOR FILING DATE: December 16, 1998
; ,, PRIOR APPLICATION NUMBER: 60/113,296
; ,, PRIOR FILING DATE: December 22, 1998
; ,, PRIOR APPLICATION NUMBER: 60/146,222
; ,, PRIOR FILING DATE: July 28, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US98/19330
; ,, PRIOR FILING DATE: September 16, 1998
; ,, PRIOR APPLICATION NUMBER: PCT/US98/25108
; ,, PRIOR FILING DATE: December 1, 1998
; ,, PRIOR APPLICATION NUMBER: 09/216,021
; ,, PRIOR FILING DATE: December 16, 1998
; ,, PRIOR APPLICATION NUMBER: 09/218,517
; ,, PRIOR FILING DATE: December 22, 1998
; ,, PRIOR APPLICATION NUMBER: 09/254,311
; ,, PRIOR FILING DATE: March 3, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US99/12252
; ,, PRIOR FILING DATE: June 22, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US99/21090
; ,, PRIOR FILING DATE: September 15, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US99/28409
; ,, PRIOR FILING DATE: No. 6936254ember 30, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US99/28313
; ,, PRIOR FILING DATE: No. 6936254ember 30, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US99/28301
; ,, PRIOR FILING DATE: December1, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US99/30095
; ,, PRIOR FILING DATE: December 16, 1999
; ,, PRIOR APPLICATION NUMBER: PCT/US00/03565

Query Match   100.0%;   Score 2211; DB 2;   Length 431;
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db   181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy   241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAAATLQAMATT 300
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Db   421 DYLINGIYVDI 431

RESULT 7
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; Sequence 83, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin
;   APPLICANT: Botstein,David
;   APPLICANT: Eaton,Dan
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gerritsen,Mary
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul
;   APPLICANT: Grimaldi,Christopher

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;   PRIOR FILING DATE: February 11, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/04414
;   PRIOR FILING DATE: February 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/05841
;   PRIOR FILING DATE: March 2, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/08439
;   PRIOR FILING DATE: March 30, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/14042
;   PRIOR FILING DATE: May 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/20710
;   PRIOR FILING DATE: July 28, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/32678
;   PRIOR FILING DATE: December 1, 2000
;   PRIOR APPLICATION NUMBER: PCT/US01/06520
;   PRIOR FILING DATE: February 28, 2001
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;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-945-587-83

Query Match             100.0%;  Score 2211; DB 2;  Length 431;
Best Local Similarity   100.0%;  Pred. No. 1.4e-201;
Matches 431; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy   181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Qy   361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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RESULT 8
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;   GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT:  Baker,Kevin P.
;   APPLICANT:  Botstein,David
;   APPLICANT:  Desnoyers,Luc
;   APPLICANT:  Eaton,Dan L.
;   APPLICANT:  Ferrara,Napoleone
;   APPLICANT:  Fong,Sherman
;   APPLICANT:  Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
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;   APPLICANT:  Goddard,Audrey
;   APPLICANT:  Godowski,Paul J.
;   APPLICANT:  Grimaldi,J.Christopher
;   APPLICANT:  Gurney,Austin L.
;   APPLICANT:  Kljavin,Ivar J.
;   APPLICANT:  Napier,Mary A.
;   APPLICANT:  Pan,James
;   APPLICANT:  Paoni,Nicholas F.
;   APPLICANT:  Roy, Margaret Ann
;   APPLICANT:  Stewart, Timothy A.
;   APPLICANT:  Tumas, Daniel
;   APPLICANT:  Watanabe, Colin K.
;   APPLICANT:  Williams, P. Mickey
;   APPLICANT:  Wood, William I.
;   APPLICANT:  Zhang, Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2730P1C27
;   CURRENT APPLICATION NUMBER: US/09/997,333
;   CURRENT FILING DATE: 2001-11-15
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;   PRIOR FILING DATE: 1997-06-16
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;   PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091626
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-09
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Query Match       100.0%;     Score 2211;  DB 2;  Length 431;
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Db  121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy  181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Qy  301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
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Db       361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420

Qy       421 DYLINGIYVDI 431
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RESULT 9
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; Sequence 515, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Botstein,David
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Eaton,Dan L.
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Fong,Sherman
;   APPLICANT: Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Grimaldi,J.Christopher
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Kljavin,Ivar J.
;   APPLICANT: Napier,Mary A.
;   APPLICANT: Pan,James
;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy,Margaret Ann
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K.
;   APPLICANT: Williams,P. Mickey
;   APPLICANT: Wood,William I.
;   APPLICANT: Zhang,Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
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;   CURRENT FILING DATE:      2001-11-14
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RESULT 10
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; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
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; PRIOR FILING DATE: 1997-06-16
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RESULT 11
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; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
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; TITLE OF INVENTION: Acids Encoding the Same
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;   PRIOR APPLICATION NUMBER: 60/092182
;   PRIOR FILING DATE: 1998-07-09
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Db          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEBDVVIDIQSSLSKGIRGNEPVTVTSTQ 60

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Db         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120

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Db        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
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Db        181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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RESULT 12
US-09-944-884-83
; Sequence 83, Application US/09944884
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; Patent No. 7018837
; GENERAL INFORMATION:
; ; APPLICANT: Baker, Kevin
; ; APPLICANT: Botstein,David
; ; APPLICANT: Eaton,Dan
; ; APPLICANT: Ferrara,Napoleone
; ; APPLICANT: Filvaroff,Ellen
; ; APPLICANT: Gerritsen,Mary
; ; APPLICANT: Goddard,Audrey
; ; APPLICANT: Godowski,Paul
; ; APPLICANT: Grimaldi,Christopher
; ; APPLICANT: Gurney,Austin
; ; APPLICANT: Hillan,Kenneth
; ; APPLICANT: Kljavin,Ivar
; ; APPLICANT: Napier,Mary
; ; APPLICANT: Roy,Margaret
; ; APPLICANT: Tumas,Daniel
; ; APPLICANT: Wood,William
; ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; ; FILE REFERENCE: P2548P1C1
; ; CURRENT APPLICATION NUMBER: US/09/944,884
; ; CURRENT FILING DATE: 2001-08-31
; ; PRIOR APPLICATION NUMBER: 09/866,028
; ; PRIOR FILING DATE: 2001-05-25
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Query Match       100.0%;  Score 2211;  DB 3;  Length 431;
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RESULT 13
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; Sequence 515, Application US/09997514
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; GENERAL INFORMATION:
; ; APPLICANT: Ashkenazi,Avi J.
; ; APPLICANT: Baker,Kevin P.
; ; APPLICANT: Botstein,David
; ; APPLICANT: Desnoyers,Luc
; ; APPLICANT: Eaton,Dan L.
; ; APPLICANT: Ferrara,Napoleone
; ; APPLICANT: Fong,Sherman
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; ; APPLICANT: Goddard,Audrey
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; ; APPLICANT: Gurney,Austin L.
; ; APPLICANT: Kljavin,Ivar J.
; ; APPLICANT: Napier,Mary A.
; ; APPLICANT: Pan,James
; ; APPLICANT: Paoni,Nicholas F.
; ; APPLICANT: Roy, Margaret Ann
; ; APPLICANT: Stewart, Timothy A.
; ; APPLICANT: Tumas,Daniel
; ; APPLICANT: Watanabe, Colin K.
; ; APPLICANT: Williams, P. Mickey
; ; APPLICANT: Wood, William I.
; ; APPLICANT: Zhang, Zemin
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PRIOR APPLICATION NUMBER: 60/092182
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PRIOR FILING DATE: 1998-07-09

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Best Local Similarity   100.0%;   Pred. No. 1.4e-201;
Matches 431;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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Db   121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy   181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR  360
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; Patent No. 7029873
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT: Baker,Kevin P.
;  APPLICANT: Botstein,David
;  APPLICANT: Desnoyers,Luc
;  APPLICANT: Eaton,Dan L.
;  APPLICANT: Ferrara,Napoleone
;  APPLICANT: Fong,Sherman
;  APPLICANT: Gerber,Hanspeter
;  APPLICANT: Gerritsen,Mary E.
;  APPLICANT: Goddard,Audrey
;  APPLICANT: Godowski,Paul J.
;  APPLICANT: Grimaldi,J.Christopher
;  APPLICANT: Gurney,Austin L.
;  APPLICANT: Kljavin,Ivar J.
;  APPLICANT: Napier,Mary A.
;  APPLICANT: Pan,James
;  APPLICANT: Paoni,Nicholas F.
;  APPLICANT: Roy, Margaret Ann
;  APPLICANT: Stewart, Timothy A.
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Watanabe, Colin K.
;  APPLICANT: Williams, P. Mickey
;  APPLICANT: Wood, William I.
;  APPLICANT: Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION: Acids Encoding the Same
;  FILE REFERENCE: P2730P1C72
;  CURRENT APPLICATION NUMBER: US/09/989,728
;  CURRENT FILING DATE: 2001-11-20
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; Sequence 515, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC37
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; CURRENT FILING DATE: 2001-11-15
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Qy   361  EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420
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Qy   421  DYLINGIYVDI  431
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          Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2211	100.0	431	3	US-09-866-028-83	Sequence 83, Appl
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3	2211	100.0	431	3	US-09-989-723-515	Sequence 515, App
4	2211	100.0	431	3	US-09-989-279-515	Sequence 515, App
5	2211	100.0	431	3	US-09-989-727-515	Sequence 515, App
6	2211	100.0	431	3	US-09-944-449-83	Sequence 83, Appl
7	2211	100.0	431	3	US-09-989-731-515	Sequence 515, App
8	2211	100.0	431	3	US-09-944-457-83	Sequence 83, Appl
9	2211	100.0	431	3	US-09-944-862-83	Sequence 83, Appl
10	2211	100.0	431	3	US-09-989-732-515	Sequence 515, App
11	2211	100.0	431	3	US-09-991-073-515	Sequence 515, App
12	2211	100.0	431	3	US-09-945-587-83	Sequence 83, Appl
13	2211	100.0	431	3	US-09-990-442-515	Sequence 515, App
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15	2211	100.0	431	3	US-09-945-015-83	Sequence 83, Appl
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18	2211	100.0	431	3	US-09-990-456-515	Sequence 515, App
19	2211	100.0	431	3	US-09-944-432-83	Sequence 83, Appl
20	2211	100.0	431	3	US-09-943-762-83	Sequence 83, Appl
21	2211	100.0	431	3	US-09-944-654-83	Sequence 83, Appl
22	2211	100.0	431	3	US-09-989-721-515	Sequence 515, App
23	2211	100.0	431	3	US-09-943-851A-83	Sequence 83, Appl
24	2211	100.0	431	3	US-09-944-413-83	Sequence 83, Appl
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665	US-09-840-746-20	3	528	6.2	137	Sequence 20, Appl
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671	US-11-443-428A-1031041	6	2987	6.2	136	Sequence 1031041,
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680	US-11-443-428A-818662	6	2263	6.1	135.5	Sequence 818662,
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688	135.5	6.1	2405	6	US-11-443-428A-818683	Sequence 818683,
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690	135.5	6.1	2487	6	US-11-443-428A-818682	Sequence 818682,
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692	135.5	6.1	2500	6	US-11-443-428A-818686	Sequence 818686,
693	135.5	6.1	2556	6	US-11-443-428A-818681	Sequence 818681,
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695	135.5	6.1	2701	4	US-10-171-311-83	Sequence 83, Appl
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708	135	6.1	497	6	US-11-443-428A-790056	Sequence 790056,
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715	134.5	6.1	1506	6	US-11-443-428A-766606	Sequence 766606,
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718	134	6.1	634	4	US-10-425-115-304196	Sequence 304196,
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767	129	5.8	3222	US-11-443-428A-921733	Sequence 921733,
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SUMMARIES

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96	2211	100.0	431	4	US-10-677-471-83	Sequence 83, Appl
97	2211	100.0	431	4	US-10-677-669-83	Sequence 83, Appl
98	2211	100.0	431	5	US-10-735-014-83	Sequence 83, Appl
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603	150.5	6.8	12756	6	US-11-066-316A-964	Sequence 964, App
604	150.5	6.8	12759	6	US-11-066-316A-959	Sequence 959, App
605	150.5	6.8	13888	6	US-11-066-316A-963	Sequence 963, App
606	150	6.8	450	6	US-11-443-428A-754578	Sequence 754578,
607	149.5	6.8	2529	6	US-11-443-428A-1030986	Sequence 1030986,
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615	149.5	6.8	5179	3	US-09-922-217-1068	Sequence 1068, Ap
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627	148	6.7	1145	6	US-11-443-428A-766604	Sequence 766604,
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636	144.5	6.5	1460	4	US-10-295-027-428	Sequence 428, App
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643	143	6.5	4	626	US-10-047-539-2	Sequence 2, Appli
644	143	6.5	5	648	US-10-565-646-6	Sequence 6, Appli
645	143	6.5	5	649	US-10-565-646-2	Sequence 2, Appli
646	143	6.5	5	649	US-10-565-646-4	Sequence 4, Appli
647	143	6.5	3	1325	US-09-864-761-35612	Sequence 35612, A
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649	142.5	6.4	4	377	US-10-312-352-30	Sequence 30, Appl
650	142.5	6.4	6	377	US-11-443-428A-766286	Sequence 766286,
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661	137.5	6.2	4	841	US-10-467-490-2	Sequence 2, Appli
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697	135.5	6.1	4	2701	US-11-510-530-83	Sequence 83, Appl
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725	133	6.0	4	1075	US-10-369-493-22068	Sequence 22068, A
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744	131.5	5.9	5	5317	US-11-715-725-59	Sequence 59, Appl
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804	128	5.8	605	5	US-10-309-407-428	Sequence 428, App
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806	128	5.8	1989	6	US-11-520-715-63112	Sequence 63112, A
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844	127	5.7	288	4	US-10-321-856-341	Sequence 341, App
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846	127	5.7	288	6	US-11-321-421-341	Sequence 341, App
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848	127	5.7	357	3	US-10-776-989-8	Sequence 8, Appli
849	127	5.7	1322	6	US-09-801-368-114	Sequence 114, App
850	127	5.7	1322	6	US-10-369-493-1353	Sequence 1353, Ap
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852	127	5.7	1469	6	US-10-990-328-9188	Sequence 9188, Ap
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857	126.5	5.7	1527	4	US-10-437-421-23	Sequence 23, Appli
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1368	114	5.2	682	4	US-10-732-923-13054	Sequence 13054,
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OM protein - protein search, using sw model

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	128.5	5.8	234	7	US-11-561-363-120	Sequence 120, App
3	126	5.7	878	7	US-11-524-253-2	Sequence 2, Appli
4	121	5.5	365	7	US-11-713-768-81599	Sequence 81599, A
5	121	5.5	402	7	US-11-713-768-81598	Sequence 81598, A
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7	117.5	5.3	907	7	US-11-561-363-60	Sequence 60, Appli
8	117	5.3	560	6	US-10-593-213-6	Sequence 6, Appli
9	116.5	5.3	1038	6	US-10-567-764-15	Sequence 15, Appl
10	116.5	5.3	792	7	US-11-713-768-81418	Sequence 81418, A
11	115.5	5.2	802	7	US-11-713-768-81417	Sequence 81417, A
12	115.5	5.2	1055	7	US-11-713-768-81416	Sequence 81416, A
13	115	5.2	981	6	US-10-567-764-7	Sequence 7, Appli
14	114	5.2	323	7	US-11-713-768-81600	Sequence 81600, A
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16	113.5	5.1	543	6	US-10-594-266-46	Sequence 46, Appl
17	113	5.1	522	6	US-10-533-069-302	Sequence 302, App
18	112	5.1	1069	6	US-10-567-764-19	Sequence 19, Appl
19	112	5.1	1100	6	US-10-567-764-23	Sequence 23, Appl
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21	111	5.0	310	7	US-11-552-437-228	Sequence 228, App
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36	106	4.8	680	7	US-11-713-768-50712	Sequence 50712, A
37	106	4.8	756	7	US-11-713-768-89081	Sequence 89081, A
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52	102	4.6	652	7	US-11-713-768-34072	Sequence 34072, A
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88	98	4.4	896	7	US-11-713-768-73161	Sequence 73161, A
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426	84.5	3.8	356	7	US-11-713-768-29846	Sequence 29846, A
427	84.5	3.8	356	7	US-11-713-768-33436	Sequence 33436, A
428	84.5	3.8	356	7	US-11-713-768-36391	Sequence 36391, A
429	84.5	3.8	387	7	US-11-728-567-12	Sequence 12, Appl
430	84.5	3.8	487	7	US-11-561-363-32	Sequence 32, Appl
431	84.5	3.8	755	7	US-11-649-663A-5004	Sequence 5004, Ap
432	84.5	3.8	772	7	US-11-713-768-83692	Sequence 83692, A
433	84.5	3.8	788	7	US-11-713-768-83691	Sequence 83691, A
434	84.5	3.8	997	7	US-11-407-888-4404	Sequence 4404, Ap
435	84.5	3.8	1244	7	US-11-407-888-84	Sequence 84, Appl
436	84.5	3.8	1319	6	US-10-438-246-19753	Sequence 19753, A
437	84.5	3.8	1491	7	US-11-649-663A-382	Sequence 382, App
438	84.5	3.8	2978	6	US-10-438-246-19493	Sequence 19493, A
439	84.5	3.8	3149	7	US-11-561-363-32	Sequence 32, Appl
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442	84	3.8	299	7	US-11-713-768-45414	Sequence 45414, A
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445	84	3.8	321	6	US-10-438-246-16060	Sequence 16060, A
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447	84	3.8	362	6	US-10-438-246-17346	Sequence 17346, A
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449	84	3.8	428	6	US-10-533-069-2351	Sequence 2351, Ap
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452	84	3.8	510	7	US-11-713-768-37331	Sequence 37331, A
453	84	3.8	561	7	US-11-713-768-36603	Sequence 36603, A
454	84	3.8	561	7	US-11-713-768-37330	Sequence 37330, A
455	84	3.8	562	6	US-10-533-069-1198	Sequence 1198, Ap
456	84	3.8	562	7	US-11-713-768-91382	Sequence 91382, A
457	84	3.8	584	7	US-11-713-768-95138	Sequence 95138, A
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462	84	3.8	765	7	US-11-713-768-96123	Sequence 96123, A
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466	84	3.8	1784	6	US-10-438-246-25818	Sequence 25818, A
467	83.5	3.8	168	7	US-11-713-768-62354	Sequence 62354, A
468	83.5	3.8	247	7	US-11-713-768-64487	Sequence 64487, A
469	83.5	3.8	328	7	US-11-257-477-155	Sequence 155, App
470	83.5	3.8	348	7	US-11-257-477-153	Sequence 153, App
471	83.5	3.8	385	7	US-11-257-477-159	Sequence 159, App
472	83.5	3.8	397	7	US-11-713-768-45827	Sequence 45827, A
473	83.5	3.8	406	7	US-11-713-768-37539	Sequence 37539, A
474	83.5	3.8	552	7	US-11-713-768-32718	Sequence 32718, A
475	83.5	3.8	558	7	US-11-713-768-47150	Sequence 47150, A
476	83.5	3.8	558	7	US-11-713-768-108588	Sequence 108588,
477	83.5	3.8	558	7	US-11-713-768-108596	Sequence 108596, A
478	83.5	3.8	559	7	US-11-713-768-47149	Sequence 47149, A
479	83.5	3.8	559	7	US-11-713-768-108587	Sequence 108587,
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481	83.5	3.8	587	7	US-11-713-768-47148	Sequence 47148, A
482	83.5	3.8	587	7	US-11-713-768-108586	Sequence 108586, A
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488	83.5	3.8	719	6	US-10-438-246-24637	Sequence 24637, A
489	83.5	3.8	733	7	US-11-713-768-85117	Sequence 85117, A
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493	83.5	3.8	1246	7	US-11-713-768-91324	Sequence 91324, A
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495	83.5	3.8	1273	7	US-11-713-768-91323	Sequence 91323, A
496	83.5	3.8	1273	7	US-11-713-768-95079	Sequence 95079, A
497	83.5	3.8	1281	7	US-11-713-768-91322	Sequence 91322, A
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508	83	3.8	423	7	US-11-551-744-196	Sequence 196, App
509	83	3.8	524	7	US-11-713-768-46472	Sequence 46472, A
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526	83	3.8	911	7	US-11-713-768-100944	Sequence 100944, A
527	83	3.8	1071	7	US-11-713-768-80594	Sequence 80594, A
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529	83	3.8	1454	6	US-10-438-246-19767	Sequence 19767, Ap
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532	82.5	3.7	185	7	US-11-713-768-21150	Sequence 21150, A
533	82.5	3.7	297	7	US-11-713-768-66249	Sequence 66249, A
534	82.5	3.7	300	7	US-11-713-768-57288	Sequence 57288, A
535	82.5	3.7	332	7	US-11-713-768-57287	Sequence 57287, A
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540	82.5	3.7	481	US-11-713-768-15048	7	Sequence 15048, A
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543	82.5	3.7	609	US-11-713-768-77317	7	Sequence 77317, A
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563	82.5	3.7	1972	US-11-649-663A-2738	7	Sequence 2738, Ap
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573	82	3.7	380	US-11-713-768-62922	7	Sequence 62922, A
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576	82	3.7	426	US-10-438-246-24118	6	Sequence 24118, A
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582	82	3.7	558	US-11-558-268-11	7	Sequence 11, Appl
583	82	3.7	598	US-11-552-437-104	7	Sequence 104, App
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589	82	3.7	1405	US-11-649-663A-2620	7	Sequence 2620, Ap
590	82	3.7	1413	US-11-649-663A-2098	7	Sequence 2098, Ap
591	82	3.7	1494	US-11-649-663A-820	7	Sequence 820, App
592	82	3.7	1910	US-11-649-663A-2256	7	Sequence 2256, Ap
593	81.5	3.7	259	US-11-603-913-9	7	Sequence 9, Appli
594	81.5	3.7	327	US-11-552-437-236	7	Sequence 236, App
595	81.5	3.7	381	US-10-438-246-33308	6	Sequence 33308, A
596	81.5	3.7	383	US-10-438-246-33229	6	Sequence 33229, A
597	81.5	3.7	412	US-11-713-768-8069	7	Sequence 8069, Ap
598	81.5	3.7	430	US-11-649-663A-5148	7	Sequence 5148, Ap
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603	81.5	3.7	623	US-10-438-246-24169	6	Sequence 24169, A
604	81.5	3.7	633	US-10-438-246-18203	6	Sequence 18203, A
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606	81.5	3.7	714	US-11-713-768-80298	7	Sequence 80298, A
607	81.5	3.7	731	US-11-713-768-80297	7	Sequence 80297, A
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610	81.5	3.7	1044	US-10-438-246-19454	6	Sequence 19454, A
611	81.5	3.7	1205	US-10-438-246-18183	6	Sequence 18183, A
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621	81	3.7	240	US-11-713-768-59359	7	Sequence 59359, A
622	81	3.7	246	US-11-713-768-59358	7	Sequence 59358, A
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624	81	3.7	301	US-10-438-246-18590	6	Sequence 18590, A
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627	81	3.7	306	US-11-713-768-58918	7	Sequence 58918, A
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643	81	3.7	451	US-11-713-768-105478	7	Sequence 105478,
644	81	3.7	457	US-11-551-744-195	7	Sequence 195, App
645	81	3.7	457	US-11-607-348A-53	7	Sequence 53, Appl
646	81	3.7	457	US-11-503-365-9	7	Sequence 9, Appli
647	81	3.7	457	US-11-503-365-37	7	Sequence 37, Appl
648	81	3.7	498	US-11-713-768-79485	7	Sequence 79485, A
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657	81	3.7	1539	US-10-438-246-26145	7	Sequence 26145, A
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666	80.5	3.6	292	US-11-713-768-45828	7	Sequence 45828, A
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671	80.5	3.6	366	US-10-438-246-24695	6	Sequence 24695, A
672	80.5	3.6	375	US-11-713-768-45521	7	Sequence 45521, A
673	80.5	3.6	382	US-11-713-768-9042	7	Sequence 9042, Ap
674	80.5	3.6	383	US-10-438-246-4977	6	Sequence 4977, Ap
675	80.5	3.6	406	US-11-713-768-24034	7	Sequence 24034, A
676	80.5	3.6	407	US-11-713-768-4976	7	Sequence 4976, Ap
677	80.5	3.6	417	US-11-713-768-86329	7	Sequence 86329, A
678	80.5	3.6	419	US-11-713-768-45520	7	Sequence 45520, A
679	80.5	3.6	420	US-11-713-768-78804	7	Sequence 78804, A
680	80.5	3.6	460	US-11-713-768-46185	7	Sequence 46185, A
681	80.5	3.6	462	US-11-713-768-46184	7	Sequence 46184, A
682	80.5	3.6	462	US-11-713-768-82086	7	Sequence 82086, A

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683	7	3.6	80.5	468	US-11-713-768-43018	Sequence 43018, A
684	7	3.6	80.5	478	US-11-713-768-72812	Sequence 72812, A
685	7	3.6	80.5	478	US-11-713-768-86328	Sequence 86328, A
686	7	3.6	80.5	501	US-11-713-768-43017	Sequence 43017, A
687	7	3.6	80.5	514	US-11-713-768-72811	Sequence 72811, A
688	7	3.6	80.5	514	US-11-713-768-82085	Sequence 82085, A
689	7	3.6	80.5	532	US-11-713-768-111514	Sequence 111514, A
690	7	3.6	80.5	557	US-11-713-768-43016	Sequence 43016, A
691	7	3.6	80.5	558	US-11-713-768-45019	Sequence 45019, A
692	7	3.6	80.5	558	US-11-713-768-49869	Sequence 49869, A
693	7	3.6	80.5	558	US-11-713-768-108349	Sequence 108349,
694	7	3.6	80.5	559	US-11-713-768-45018	Sequence 45018, A
695	7	3.6	80.5	559	US-11-713-768-111513	Sequence 111513,
696	7	3.6	80.5	559	US-11-713-768-108348	Sequence 108348,
697	7	3.6	80.5	561	US-11-713-768-49868	Sequence 49868, A
698	7	3.6	80.5	587	US-11-713-768-45017	Sequence 45017, A
699	7	3.6	80.5	587	US-11-713-768-49867	Sequence 49867, A
700	7	3.6	80.5	587	US-11-713-768-108347	Sequence 108347,
701	7	3.6	80.5	601	US-11-713-768-78803	Sequence 78803, A
702	7	3.6	80.5	601	US-11-713-768-111512	Sequence 111512,
703	7	3.6	80.5	616	US-11-713-768-86327	Sequence 86327, A
704	7	3.6	80.5	626	US-11-713-768-82084	Sequence 82084, A
705	7	3.6	80.5	632	US-11-713-768-72810	Sequence 72810, A
706	7	3.6	80.5	639	US-11-395-197-38	Sequence 38, Appl
707	7	3.6	80.5	639	US-11-396-216-38	Sequence 38, Appl
708	7	3.6	80.5	658	US-11-713-768-108398	Sequence 108398,
709	7	3.6	80.5	663	US-11-713-768-108397	Sequence 108397,
710	6	3.6	80.5	791	US-10-438-246-18832	Sequence 18832, A
711	7	3.6	80.5	806	US-11-713-768-49358	Sequence 49358, A
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715	6	3.6	80.5	1740	US-10-438-246-17651	Sequence 17651, A
716	7	3.6	80.5	1783	US-11-649-663A-1440	Sequence 1440, Ap
717	7	3.6	80.5	1791	US-11-649-663A-2026	Sequence 2026, Ap
718	7	3.6	80	289	US-11-713-768-15898	Sequence 15898, A
719	6	3.6	80	301	US-10-438-246-31654	Sequence 31654, A
720	7	3.6	80	313	US-11-713-768-15897	Sequence 15897, A
721	6	3.6	80	356	US-10-438-246-8719	Sequence 8719, Ap
722	6	3.6	80	402	US-10-533-069-619	Sequence 619, App
723	6	3.6	80	414	US-10-438-246-9272	Sequence 9272, Ap
724	7	3.6	80	473	US-11-713-768-56849	Sequence 56849, A
725	6	3.6	80	484	US-10-438-246-33364	Sequence 33364, A
726	7	3.6	80	485	US-11-713-768-98714	Sequence 98714, A
727	7	3.6	80	560	US-11-713-768-16002	Sequence 16002, A
728	6	3.6	80	561	US-10-438-246-30292	Sequence 30292, A
729	6	3.6	80	746	US-10-438-246-20163	Sequence 20163, A
730	6	3.6	80	746	US-10-438-246-26116	Sequence 26116, A
731	7	3.6	80	934	US-11-713-768-82039	Sequence 82039, A
732	6	3.6	80	945	US-10-438-246-16475	Sequence 16475, A
733	6	3.6	80	962	US-10-438-246-82038	Sequence 82038, A
734	7	3.6	80	974	US-11-713-768-82037	Sequence 82037, A
735	6	3.6	80	986	US-10-438-246-32438	Sequence 32438, A
736	6	3.6	80	1454	US-10-533-069-1144	Sequence 1144, Ap
737	7	3.6	80	1628	US-11-649-663A-2748	Sequence 2748, Ap
738	6	3.6	80	1636	US-10-438-246-10007	Sequence 10007, A
739	7	3.6	80	1761	US-11-649-663A-1526	Sequence 1526, Ap
740	6	3.6	80	1839	US-10-438-246-18696	Sequence 18696, A
741	6	3.6	80	2000	US-10-533-069-1298	Sequence 1298, App
742	7	3.6	80	2147	US-11-707-223-44	Sequence 44, Appl
743	7	3.6	79.5	91	US-11-713-768-68367	Sequence 68367, A
744	7	3.6	79.5	144	US-11-713-768-18107	Sequence 18107, A
745	7	3.6	79.5	168	US-11-593-213-4	Sequence 4, Appli
746	6	3.6	79.5	262	US-10-438-246-7613	Sequence 7613, Ap
747	6	3.6	79.5	351	US-10-438-246-16176	Sequence 16176, Ap
748	6	3.6	79.5	351	US-10-438-246-23767	Sequence 23767, A
749	6	3.6	79.5	424	US-10-438-246-18616	Sequence 18616, A
750	7	3.6	79.5	439	US-11-713-768-70633	Sequence 70633, A
751	7	3.6	79.5	471	US-11-713-768-70632	Sequence 70632, A
752	6	3.6	79.5	486	US-10-438-246-9456	Sequence 9456, Ap
753	7	3.6	79.5	493	US-11-713-768-68313	Sequence 68313, A
754	7	3.6	79.5	500	US-11-713-768-68312	Sequence 68312, A
755	7	3.6	79.5	509	US-11-713-768-68311	Sequence 68311, A

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757	783	6	3.6	79.5	US-10-438-246-16209	Sequence 16209, A
758	783	6	3.6	79.5	US-10-438-246-23818	Sequence 23818, A
759	811	6	3.6	79.5	US-10-438-246-26245	Sequence 26245, A
760	901	6	3.6	79.5	US-11-407-888-119	Sequence 119, App
761	1020	6	3.6	79.5	US-10-438-246-30050	Sequence 30050, A
762	1026	7	3.6	79.5	US-11-649-663A-1518	Sequence 1518, Ap
763	1274	7	3.6	79.5	US-11-649-663A-1848	Sequence 1848, Ap
764	1282	6	3.6	79.5	US-10-438-246-17848	Sequence 17848, A
765	1282	6	3.6	79.5	US-10-438-246-25068	Sequence 25068, A
766	1357	7	3.6	79.5	US-11-649-663A-1724	Sequence 1724, Ap
767	1359	7	3.6	79.5	US-11-649-663A-974	Sequence 974, App
768	1724	6	3.6	79.5	US-10-438-246-18742	Sequence 18742, A
769	1806	6	3.6	79.5	US-10-438-246-25794	Sequence 25794, A
770	2087	7	3.6	79.5	US-10-681-649-253	Sequence 253, App
771	2188	7	3.6	79.5	US-10-572-442B-2	Sequence 2, Appli
772	185	6	3.6	79	US-11-713-768-62315	Sequence 62315, A
773	199	6	3.6	79	US-10-565-622-67	Sequence 67, Appl
774	239	7	3.6	79	US-11-713-768-21343	Sequence 21343, A
775	239	7	3.6	79	US-11-713-768-41388	Sequence 41388, A
776	239	7	3.6	79	US-11-713-768-73801	Sequence 73801, A
777	239	7	3.6	79	US-11-713-768-76931	Sequence 76931, A
778	239	7	3.6	79	US-11-713-768-106863	Sequence 106863,
779	277	7	3.6	79	US-11-713-768-29848	Sequence 29848, A
780	277	7	3.6	79	US-11-713-768-33438	Sequence 33438, A
781	277	7	3.6	79	US-11-713-768-36393	Sequence 36393, A
782	290	7	3.6	79	US-11-713-768-58107	Sequence 58107, A
783	294	7	3.6	79	US-11-713-768-40881	Sequence 40881, A
784	294	7	3.6	79	US-11-713-768-98815	Sequence 98815, A
785	295	7	3.6	79	US-11-713-768-108759	Sequence 108759,
786	303	6	3.6	79	US-10-438-246-17360	Sequence 17360, A
787	310	7	3.6	79	US-11-713-768-15753	Sequence 15753, A
788	358	7	3.6	79	US-11-713-768-70634	Sequence 70634, A
789	365	6	3.6	79	US-10-547-956-854	Sequence 854, App
790	382	6	3.6	79	US-10-438-246-6214	Sequence 6214, Ap
791	382	6	3.6	79	US-10-438-246-6215	Sequence 6215, Ap
792	385	7	3.6	79	US-11-713-768-40880	Sequence 40880, A
793	385	7	3.6	79	US-11-713-768-98814	Sequence 98814, A
794	415	6	3.6	79	US-10-438-246-32066	Sequence 32066, A
795	429	7	3.6	79	US-11-713-768-40879	Sequence 40879, A
796	429	7	3.6	79	US-11-713-768-98813	Sequence 98813, A
797	473	7	3.6	79	US-11-713-768-110507	Sequence 110507,
798	480	7	3.6	79	US-11-713-768-101821	Sequence 101821,
799	509	7	3.6	79	US-11-713-768-101820	Sequence 101820,
800	511	6	3.6	79	US-10-438-246-18136	Sequence 18136, A
801	528	6	3.6	79	US-11-725-235-126	Sequence 126, App
802	528	7	3.6	79	US-11-728-557-1076	Sequence 1076, Ap
803	528	7	3.6	79	US-11-713-768-101819	Sequence 101819,
804	550	7	3.6	79	US-11-713-768-26628	Sequence 26628, A
805	550	7	3.6	79	US-11-713-768-105174	Sequence 105174,
806	565	7	3.6	79	US-11-713-768-110506	Sequence 110506,
807	574	6	3.6	79	US-10-438-246-10779	Sequence 10779, A
808	575	7	3.6	79	US-11-713-768-26627	Sequence 26627, A
809	575	7	3.6	79	US-11-713-768-105173	Sequence 105173,
810	597	7	3.6	79	US-11-713-768-26626	Sequence 26626, A
811	597	7	3.6	79	US-11-713-768-105172	Sequence 105172,
812	624	7	3.6	79	US-11-713-768-110505	Sequence 110505,
813	658	6	3.6	79	US-10-438-246-26244	Sequence 26244, A
814	667	7	3.6	79	US-11-713-768-79910	Sequence 79910, A
815	967	7	3.6	79	US-11-713-768-86722	Sequence 86722, A
816	980	7	3.6	79	US-11-649-663A-3450	Sequence 3450, Ap
817	1036	6	3.6	79	US-10-438-246-18736	Sequence 18736, A
818	1041	6	3.6	79	US-10-438-246-25824	Sequence 25824, A
819	1192	6	3.6	79	US-10-438-246-18698	Sequence 18698, A
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821	1273	7	3.6	79	US-11-713-768-72484	Sequence 72484, A
822	1310	7	3.6	79	US-11-713-768-72483	Sequence 72483, A
823	1777	6	3.6	79	US-10-438-246-18736	Sequence 18736, A
824	1813	6	3.6	79	US-10-438-246-25824	Sequence 25824, A
825	1813	6	3.6	79	US-10-438-246-18698	Sequence 18698, A
826	2032	7	3.6	79	US-11-713-768-72485	Sequence 72485, A
827	2057	7	3.6	79	US-11-713-768-72484	Sequence 72484, A
828	2226	7	3.6	79	US-11-713-768-72483	Sequence 72483, A

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831	78.5	3.6	309	7	US-11-713-768-4664	Sequence 4664, Ap
832	78.5	3.6	309	7	US-11-713-768-9283	Sequence 9283, Ap
833	78.5	3.6	352	7	US-11-713-768-53190	Sequence 53190, A
834	78.5	3.6	375	7	US-11-713-768-98003	Sequence 98003, A
835	78.5	3.6	401	7	US-11-713-768-29234	Sequence 29234, A
836	78.5	3.6	401	7	US-11-713-768-32824	Sequence 32824, A
837	78.5	3.6	401	7	US-11-713-768-98002	Sequence 98002, A
838	78.5	3.6	401	7	US-11-713-768-99830	Sequence 99830, A
839	78.5	3.6	402	7	US-11-713-768-4663	Sequence 4663, Ap
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841	78.5	3.6	413	7	US-11-713-768-29233	Sequence 29233, A
842	78.5	3.6	413	7	US-11-713-768-32823	Sequence 32823, A
843	78.5	3.6	413	7	US-11-713-768-99829	Sequence 99829, A
844	78.5	3.6	436	7	US-11-713-768-4662	Sequence 4662, Ap
845	78.5	3.6	436	7	US-11-713-768-9281	Sequence 9281, Ap
846	78.5	3.6	442	7	US-10-438-246-18587	Sequence 18587, A
847	78.5	3.6	451	7	US-11-713-768-98001	Sequence 98001, A
848	78.5	3.6	455	6	US-10-438-246-25529	Sequence 25529, A
849	78.5	3.6	493	6	US-10-438-246-15954	Sequence 15954, A
850	78.5	3.6	498	7	US-11-796-730-2949	Sequence 2949, Ap
851	78.5	3.6	509	7	US-11-713-768-66130	Sequence 66130, A
852	78.5	3.6	529	7	US-11-713-768-66129	Sequence 66129, A
853	78.5	3.6	567	7	US-11-407-888-107	Sequence 107, App
854	78.5	3.6	594	7	US-11-713-768-66128	Sequence 66128, A
855	78.5	3.6	623	7	US-11-713-768-15460	Sequence 15460, A
856	78.5	3.6	642	6	US-10-438-246-18252	Sequence 18252, A
857	78.5	3.6	656	6	US-10-533-069-2082	Sequence 2082, Ap
858	78.5	3.6	699	7	US-11-713-768-75159	Sequence 75159, A
859	78.5	3.6	725	7	US-11-713-768-15459	Sequence 15459, A
860	78.5	3.6	746	7	US-11-713-768-75158	Sequence 75158, A
861	78.5	3.6	758	7	US-11-713-768-15458	Sequence 15458, A
862	78.5	3.6	801	6	US-10-438-246-5648	Sequence 5648, Ap
863	78.5	3.6	1333	6	US-11-649-663A-2520	Sequence 2520, Ap
864	78.5	3.6	1335	6	US-11-649-663A-2138	Sequence 2138, Ap
865	78.5	3.6	1364	6	US-10-438-246-16615	Sequence 16615, A
866	78.5	3.6	1364	7	US-10-438-246-24076	Sequence 24076, A
867	78.5	3.6	1633	7	US-11-649-663A-2704	Sequence 2704, Ap
868	78.5	3.6	1693	7	US-11-649-663A-4190	Sequence 4190, Ap
869	78.5	3.6	1972	6	US-10-533-069-396	Sequence 396, App
870	78	3.5	145	7	US-11-713-768-66018	Sequence 66018, A
871	78	3.5	178	7	US-10-565-626-62	Sequence 62, Appl
872	78	3.5	191	7	US-11-713-768-66300	Sequence 66300, A
873	78	3.5	220	7	US-11-713-768-109277	Sequence 109277,
874	78	3.5	232	7	US-11-713-768-109276	Sequence 109276,
875	78	3.5	237	6	US-10-438-246-30346	Sequence 30346, A
876	78	3.5	267	7	US-11-713-768-5049	Sequence 5049, Ap
877	78	3.5	307	7	US-11-713-768-17934	Sequence 17934, A
878	78	3.5	307	6	US-10-438-246-25130	Sequence 25130, A
879	78	3.5	309	7	US-11-713-768-19400	Sequence 19400, A
880	78	3.5	333	6	US-10-438-246-17489	Sequence 17489, A
881	78	3.5	333	6	US-10-438-246-24789	Sequence 24789, A
882	78	3.5	337	6	US-10-438-246-5047	Sequence 5047, Ap
883	78	3.5	340	7	US-11-713-768-37540	Sequence 37540, A
884	78	3.5	361	7	US-11-713-768-109269	Sequence 109269,
885	78	3.5	361	7	US-11-741-136-1	Sequence 1, Appli
886	78	3.5	401	6	US-10-438-246-25332	Sequence 25332, A
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888	78	3.5	410	7	US-11-713-768-107834	Sequence 107834,
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891	78	3.5	511	7	US-11-713-768-86641	Sequence 86641, A
892	78	3.5	541	7	US-11-713-768-75616	Sequence 75616, A
893	78	3.5	550	7	US-11-713-768-96078	Sequence 96078, A
894	78	3.5	550	7	US-11-713-768-87370	Sequence 87370, A
895	78	3.5	559	7	US-11-713-768-75615	Sequence 75615, A
896	78	3.5	573	7	US-11-713-768-87369	Sequence 87369, A
897	78	3.5	582	7	US-11-713-768-107833	Sequence 107833,
898	78	3.5	609	7	US-11-713-768-86640	Sequence 86640, A
899	78	3.5	666	6	US-10-438-246-8932	Sequence 8932, Ap
900	78	3.5	671	6	US-11-713-768-86639	Sequence 86639, A
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902	78	3.5	901	7	US-11-657-812-1	Sequence 1, Appli
903	78	3.5	999	7	US-11-649-663A-1422	Sequence 1422, Ap
904	78	3.5	1008	7	US-11-649-663A-1620	Sequence 1620, Ap
905	78	3.5	1073	7	US-11-649-663A-1312	Sequence 1312, Ap
906	78	3.5	1355	6	US-10-438-246-20693	Sequence 20693, A
907	78	3.5	2535	6	US-10-438-246-10675	Sequence 10675, A
908	78	3.5	3330	6	US-10-438-246-26097	Sequence 26097, A
909	77.5	3.5	165	7	US-11-713-768-20795	Sequence 20795, A
910	77.5	3.5	165	7	US-11-713-768-102999	Sequence 102999,
911	77.5	3.5	173	7	US-11-713-768-20794	Sequence 20794, A
912	77.5	3.5	173	7	US-11-713-768-102998	Sequence 102998,
913	77.5	3.5	177	7	US-11-713-768-20793	Sequence 20793, A
914	77.5	3.5	177	7	US-11-713-768-102997	Sequence 102997,
915	77.5	3.5	234	7	US-11-713-768-3335	Sequence 3335, Ap
916	77.5	3.5	255	7	US-11-713-768-41743	Sequence 41743, A
917	77.5	3.5	255	7	US-11-713-768-101464	Sequence 101464,
918	77.5	3.5	269	7	US-11-713-768-2619	Sequence 2619, Ap
919	77.5	3.5	302	7	US-11-713-768-49636	Sequence 49636, A
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921	77.5	3.5	336	7	US-11-713-768-28388	Sequence 28388, A
922	77.5	3.5	336	7	US-11-713-768-31978	Sequence 31978, A
923	77.5	3.5	336	7	US-11-713-768-77804	Sequence 77804, A
924	77.5	3.5	358	7	US-11-713-768-84466	Sequence 84466, A
925	77.5	3.5	358	7	US-11-713-768-3562	Sequence 3562, Ap
926	77.5	3.5	367	7	US-11-713-768-78375	Sequence 78375, A
927	77.5	3.5	374	6	US-10-438-246-31463	Sequence 31463, A
928	77.5	3.5	386	7	US-11-713-768-37570	Sequence 37570, A
929	77.5	3.5	390	7	US-11-713-768-3561	Sequence 3561, Ap
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1183	3.4	76	3395	US-10-438-246-25808	6	Sequence 25808, A
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1192	3.4	75.5	288	US-11-713-768-32437	7	Sequence 32437, A
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1345	74.5	3.4	294	7	US-11-713-768-108883	Sequence 108883,
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and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: September 19, 2007, 18:50:34 ; Search time 739 Seconds
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	2211	100.0	431	26	US-09-629-469A-17950	Sequence 17950, A
5	2211	100.0	431	29	US-09-929-404-72	Sequence 72, Appl
6	2211	100.0	431	29	US-09-941-992-515	Sequence 515, App
7	2211	100.0	431	29	US-09-943-564-83	Sequence 83, Appl
8	2211	100.0	431	29	US-09-943-762-83	Sequence 83, Appl
9	2211	100.0	431	29	US-09-943-780-83	Sequence 83, Appl
10	2211	100.0	431	29	US-09-943-851-83	Sequence 83, Appl
11	2211	100.0	431	29	US-09-943-851A-83	Sequence 83, Appl
12	2211	100.0	431	29	US-09-944-396-83	Sequence 83, Appl
13	2211	100.0	431	29	US-09-944-403-83	Sequence 83, Appl
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15	2211	100.0	431	29	US-09-944-432-83	Sequence 83, Appl
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19	2211	100.0	431	29	US-09-944-862-83	Sequence 83, Appl
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21	2211	100.0	431	29	US-09-944-929-83	Sequence 83, Appl
22	2211	100.0	431	29	US-09-945-015-83	Sequence 83, Appl
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589	188	8.5	449	43	US-11-371-354-12350	Sequence 12350, A
590	188	8.5	449	43	US-11-371-354-57983	Sequence 57983, A
591	188	8.5	449	43	US-11-371-354-76166	Sequence 76166, A
592	188	8.5	449	45	US-11-537-235-224	Sequence 224, App
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594	187.5	8.5	417	23	US-09-358-001-16	Sequence 16, Appl
595	187.5	8.5	417	25	US-09-578-334-16	Sequence 16, Appl
596	187.5	8.5	417	25	US-09-578-334B-16	Sequence 16, Appl
597	187.5	8.5	417	25	US-09-578-517-16	Sequence 16, Appl
598	187.5	8.5	417	25	US-09-578-518-16	Sequence 16, Appl
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602	187.5	8.5	417	25	US-09-578-520-16	Sequence 16, Appl
603	187.5	8.5	417	25	US-09-578-520B-16	Sequence 16, Appl
604	187.5	8.5	417	25	US-09-578-831B-16	Sequence 16, Appl
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610	187.5	8.5	417	25	US-09-579-280-16	Sequence 16, Appl
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612	184.5	8.3	322	44	US-11-443-428A-754581	Sequence 754581,
613	183	8.3	266	1	PCT-US99-17130-322	Sequence 322, App
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616	178.5	8.1	289	44	US-11-443-428A-754590	Sequence 754590,
617	163	7.4	4262	58	US-60-836-986-25063	Sequence 25063, A
618	162	7.3	2839	42	US-11-222-045-1973	Sequence 1973, Ap
619	162	7.3	2839	44	US-11-475-062-6111	Sequence 6111, Ap
620	162	7.3	2839	56	US-60-651-508-231	Sequence 231, App
621	161	7.3	5416	56	US-60-680-003-420	Sequence 420, App
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628	157.5	7.1	2448	45	US-11-582-861-10455	Sequence 10455, A
629	157.5	7.1	2448	57	US-60-763-373-49	Sequence 49, Appl
630	156.5	7.1	343	1	PCT-US02-05095A-1360	Sequence 1360, Ap
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634	152.5	6.9	22152	1	PCT-US03-37041-5	Sequence 5, Appl
635	152.5	6.9	22152	34	US-10-475-117-315	Sequence 315, App
636	150.5	6.8	334	37	US-10-715-066A-5	Sequence 5, Appli
637	150.5	6.8	334	43	US-11-360-355-120669	Sequence 120669,
638	150.5	6.8	860	56	US-60-655-875-120669	Sequence 120669,
639	150.5	6.8	860	1	PCT-US05-43512-3	Sequence 3, Appli
640	150.5	6.8	860	27	US-09-791-537-54719	Sequence 54719, A
641	150.5	6.8	860	27	US-09-791-537-116549	Sequence 116549,
642	150.5	6.8	860	42	US-11-292-431-3	Sequence 3, Appli
643	150.5	6.8	7180	31	US-10-170-205E-12427	Sequence 12427, A
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645	150.5	6.8	12704	40	US-11-066-316A-960	Sequence 960, App
646	150.5	6.8	12756	40	US-11-066-316A-964	Sequence 964, App
647	150.5	6.8	12759	40	US-11-066-316A-959	Sequence 959, App
648	150	6.8	13888	44	US-11-066-316A-963	Sequence 963, App
649	150	6.8	450	44	US-11-443-428A-754578	Sequence 754578,
650	149.5	6.8	247	26	US-09-641-377-705	Sequence 705, App
651	149.5	6.8	260	26	US-09-641-377-700	Sequence 700, App
652	149.5	6.8	277	26	US-09-641-377-704	Sequence 704, App
653	149.5	6.8	368	26	US-09-641-377-699	Sequence 699, App
654	149.5	6.8	385	26	US-09-641-377-698	Sequence 698, App
655	149.5	6.8	386	26	US-09-641-377-701	Sequence 701, App
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658	149.5	6.8	717	26	US-09-641-377-686	Sequence 686, App
659	149.5	6.8	1270	27	US-09-791-537-121899	Sequence 121899,
660	149.5	6.8	2529	44	US-11-443-428A-1030986	Sequence 1030986,
661	149.5	6.8	2785	44	US-11-443-428A-1030985	Sequence 1030985,
662	149.5	6.8	2892	44	US-11-443-428A-1030989	Sequence 1030989,
663	149.5	6.8	2931	44	US-11-443-428A-1030987	Sequence 1030987,
664	149.5	6.8	3208	44	US-11-443-428A-1030984	Sequence 1030984,
665	149.5	6.8	3215	44	US-11-443-428A-1030988	Sequence 1030988,
666	149.5	6.8	3292	44	US-11-443-428A-1030982	Sequence 1030982,
667	149.5	6.8	3570	31	US-10-109-346C-36107	Sequence 36107, A
668	149.5	6.8	3570	31	US-10-109-346C-36110	Sequence 36110, A
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673	149.5	6.8	4315	34	US-10-461-673-9612	Sequence 9612, A
674	149.5	6.8	4742	32	US-10-221-279-12349	Sequence 12349, A
675	149.5	6.8	5178	37	PCT-US04-36404-178	Sequence 178, App
676	149.5	6.8	5178	1	US-10-700-439-178	Sequence 178, App
677	149.5	6.8	5179	1	PCT-US02-11475A-1068	Sequence 1068, Ap
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679	149.5	6.8	5179	1	PCT-US05-26647A-185	Sequence 185, App
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682	149.5	6.8	5179	26	US-09-649-811-1068	Sequence 1068, Ap
683	149.5	6.8	5179	28	US-10-461-673-1068	Sequence 1068, Ap
684	149.5	6.8	5179	29	US-09-833-263-1068	Sequence 1068, Ap
685	149.5	6.8	5179	29	US-09-922-217-1068	Sequence 1068, Ap
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687	149.5	6.8	5179	30	US-10-025-380-1068	Sequence 1068, Ap
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689	149.5	6.8	5179	32	US-10-219-051B-10430	Sequence 10430, A
690	149.5	6.8	5179	32	US-10-219-051B-13789	Sequence 13789, A
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693	149.5	6.8	5179	41	US-11-105-233-185	Sequence 185, App
694	149.5	6.8	5179	41	US-11-108-172-1068	Sequence 1068, Ap
695	149.5	6.8	5179	42	US-11-222-045-1120	Sequence 1120, Ap
696	149.5	6.8	5179	43	US-11-426-161-1180	Sequence 1180, Ap
697	149.5	6.8	5179	44	US-11-437-729-1766	Sequence 1766, Ap
698	149.5	6.8	5179	44	US-11-443-428A-1030981	Sequence 1030981,
699	149.5	6.8	5179	44	US-11-475-062-2277	Sequence 2277, Ap
700	149.5	6.8	5179	47	US-11-721-099-2	Sequence 2, Appli
701	149.5	6.8	5179	54	US-60-438-735-151	Sequence 151, App
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708	149.5	6.8	5703	44	US-11-426-161-1181	Sequence 1181, App
709	149.5	6.8	5703	44	US-11-475-062-2747	Sequence 2747, Ap
710	149.5	6.8	5703	44	US-11-490-374-756	Sequence 756, App
711	149.5	6.8	5703	45	US-11-582-861-5598	Sequence 5598, Ap
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713	149.5	6.8	5703	56	US-60-636-720-901	Sequence 901, App
714	149.5	6.8	5703	57	US-60-701-057-161	Sequence 161, App
715	149	6.8	2905	31	US-10-170-205E-15818	Sequence 15818, A
716	148.5	6.7	1233	35	US-10-544-731A-11	Sequence 11, Appl
717	148.5	6.7	1233	45	US-11-582-861-8312	Sequence 8312, Ap
718	148.5	6.7	1233	47	US-11-721-099-3	Sequence 3, Appli
719	148.5	6.7	1233	57	US-60-763-373-64	Sequence 64, Appl
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721	148	6.7	2051	44	US-11-443-428A-766608	Sequence 766608,
722	148	6.7	2205	44	US-11-443-428A-766601	Sequence 766601,
723	147.5	6.7	1609	33	US-10-369-493-1535	Sequence 1535, Ap
724	147.5	6.7	1609	53	US-10-360-039-1535	Sequence 1535, Ap
725	147	6.6	662	27	US-09-791-537-81398	Sequence 81398, A
726	147	6.6	811	44	US-11-443-428A-869930	Sequence 869930,
727	147	6.6	4152	31	US-10-170-205E-31645	Sequence 31645, A
728	146.5	6.6	1393	52	US-60-242-679-1481	Sequence 1481, Ap
729	146	6.6	174	51	US-60-196-190-1445	Sequence 1445, Ap
730	146	6.6	472	57	US-60-752-355-42245	Sequence 42245, A
731	146	6.6	786	27	US-09-791-537-65885	Sequence 65885, A
732	145.5	6.6	716	56	US-60-608-498-660	Sequence 660, App
733	145	6.6	747	1	PCT-US04-21492-134	Sequence 134, App
734	145	6.6	747	1	PCT-US04-21492A-134	Sequence 134, App
735	145	6.6	747	1	PCT-US06-46919-118	Sequence 118, App
736	145	6.6	747	1	PCT-US07-04429-414	Sequence 414, App
737	145	6.6	747	35	US-10-560-957-134	Sequence 134, App
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741	145	6.6	2109	1	PCT-US04-10531-92	Sequence 92, Appl
742	145	6.6	2254	1	PCT-US04-10531-93	Sequence 93, Appl
743	145	6.6	2401	1	PCT-US04-10531-94	Sequence 94, Appl
744	144.5	6.5	377	43	US-11-371-354-56047	Sequence 56047, A
745	144.5	6.5	377	58	US-60-836-986-24532	Sequence 24532, A
746	144.5	6.5	505	44	US-11-443-428A-1025293	Sequence 105293,
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748	144.5	6.5	764	51	US-60-167-324-293	Sequence 293, App
749	144.5	6.5	764	51	US-60-173-386-275	Sequence 275, App
750	144.5	6.5	764	51	US-60-175-871-320	Sequence 320, App
751	144.5	6.5	787	26	US-09-614-150A-40698	Sequence 40698, A
752	144.5	6.5	787	26	US-09-614-150A-40698	Sequence 40698, A
753	144.5	6.5	787	27	US-09-791-537-124063	Sequence 124063,
754	144.5	6.5	787	40	US-11-097-143-40698	Sequence 40698, A
755	144.5	6.5	787	51	US-60-184-775-285	Sequence 285, App
756	144.5	6.5	787	51	US-60-191-637-40323	Sequence 40323, A
757	144.5	6.5	787	51	US-60-191-700-309	Sequence 309, App
758	144.5	6.5	1139	44	US-11-443-428A-924025	Sequence 924025,
759	144.5	6.5	1370	1	PCT-US02-29964-917	Sequence 917, APP
760	144.5	6.5	1370	34	US-10-461-673-17041	Sequence 17041, A
761	144.5	6.5	1460	32	US-10-295-027-428	Sequence 428, App
762	144.5	6.5	1538	1	PCT-US02-29964-453	Sequence 453, APP
763	144.5	6.5	1538	34	US-10-461-673-16797	Sequence 16797, A
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766	144	6.5	849	44	US-11-443-428A-765734	Sequence 765734,
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768	144	6.5	10431	1	PCT-US02-11734-310	Sequence 310, App
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770	144	6.5	10431	54	US-60-427-045-310	Sequence 310, App
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772	144	6.5	14507	58	US-60-836-986-31920	Sequence 31920, A
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780	143.5	143.5	6.5	916	US-10-179-131-6093	31	Sequence 6093, Ap
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790	143	143	6.5	1325	US-10-182-995-22084	31	Sequence 22084, A
791	143	143	6.5	1325	US-10-182-998-12385	31	Sequence 12385, A
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793	143	143	6.5	1325	US-10-203-135-27277	32	Sequence 27277, A
794	143	143	6.5	1325	US-10-203-136-28383	32	Sequence 28383, A
795	143	143	6.5	1325	US-10-203-138-12693	32	Sequence 12693, A
796	143	143	6.5	1325	US-10-203-138A-12693	32	Sequence 12693, A
797	143	143	6.5	1325	US-10-203-139-27532	32	Sequence 27532, A
798	143	143	6.5	1325	US-60-236-359-17299	52	Sequence 17299, A
799	143	143	6.5	4295	US-11-490-374-755	44	Sequence 755, App
800	143	143	6.5	4295	US-11-721-099-4	47	Sequence 4, Appli
801	143	143	6.5	4295	US-60-701-057-160	57	Sequence 160, App
802	142.5	142.5	6.4	1	PCT-US00-32290-7	1	Sequence 7, Appli
803	142.5	142.5	6.4	377	US-10-149-819-7	31	Sequence 7, Appli
804	142.5	142.5	6.4	377	US-10-170-205E-20391	31	Sequence 20391, A
805	142.5	142.5	6.4	377	US-10-312-352-30	33	Sequence 30, Appl
806	142.5	142.5	6.4	377	US-11-443-428A-766286	44	Sequence 766286,
807	142.5	142.5	6.4	377	US-60-191-637-39640	51	Sequence 39640, A
808	142.5	142.5	6.4	866	US-09-791-537-93418	27	Sequence 93418, A
809	142.5	142.5	6.4	866	US-10-626-832-86	36	Sequence 86, Appl
810	142.5	142.5	6.4	1440	US-11-443-428A-766602	44	Sequence 766602,
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813	142	142	6.4	875	US-09-614-150-40008	26	Sequence 40008, A
814	142	142	6.4	875	US-09-614-150A-40008	26	Sequence 40008, A
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816	142	142	6.4	875	US-60-191-637-39640	51	Sequence 39640, A
817	142	142	6.4	875	US-60-191-681-30670	51	Sequence 30670, A
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828	139.5	139.5	6.3	562	US-11-443-428A-1034203	44	Sequence 1034203,
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830	139	139	6.3	2264	US-60-164-769-17377	51	Sequence 17377, A
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1099	129	5.8	365	1	PCT-US07-62986-28	Sequence 28, Appl
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1197	129	5.8	1859	27	US-09-724-676-50771	Sequence 50771, A
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1207	129	5.8	1906	31	US-10-109-346C-13028	Sequence 13028, A
1208	129	5.8	1906	31	US-10-109-346C-13034	Sequence 13034, A
1209	129	5.8	1924	27	US-09-724-676-50777	Sequence 50777, A
1210	129	5.8	1924	27	US-09-724-676A-50777	Sequence 50777, A
1211	129	5.8	1926	27	US-09-724-676-50778	Sequence 50778, A
1212	129	5.8	1926	27	US-09-724-676A-50778	Sequence 50778, A
1213	129	5.8	1939	27	US-09-724-676-50841	Sequence 50841, A
1214	129	5.8	1939	27	US-09-724-676A-50841	Sequence 50841, A
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1219	129	5.8	2011	31	US-10-109-346C-13031	Sequence 13031, A
1220	129	5.8	2011	31	US-10-109-346C-13036	Sequence 13036, A
1221	129	5.8	2011	34	US-10-408-765A-767	Sequence 767, App
1222	129	5.8	2011	34	US-10-408-765A-767	Sequence 767, App
1223	129	5.8	2011	53	US-10-389-987-767	Sequence 767, App
1224	129	5.8	2011	54	US-60-412-418-767	Sequence 767, App
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1231	129	5.8	3014	44	US-11-475-062-582	Sequence 582, App
1232	129	5.8	3014	56	US-60-636-720-504	Sequence 504, App
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1240	129	5.8	3360	44	US-11-475-062-586	Sequence 586, App
1241	129	5.8	3360	44	US-60-636-720-508	Sequence 508, App
1242	129	5.8	3360	56	US-60-636-720-510	Sequence 510, App
1243	129	5.8	3361	45	US-11-582-861-6033	Sequence 6033, Ap
1244	129	5.8	3391	44	US-11-443-428A-921722	Sequence 921722,
1245	129	5.8	3404	44	US-11-443-428A-921763	Sequence 921763,
1246	129	5.8	3406	44	US-11-443-428A-921752	Sequence 921752,
1247	129	5.8	3471	44	US-11-443-428A-921716	Sequence 921716,
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1253	129	5.8	3637	44	US-11-443-428A-921757	Sequence 921757,
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1257	129	5.8	3698	44	US-11-475-062-583	Sequence 583, App
1258	129	5.8	3698	56	US-60-636-720-506	Sequence 506, App
1259	129	5.8	3698	56	US-60-636-720-509	Sequence 509, App
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1266	129	5.8	3759	44	US-11-443-428A-921762	Sequence 921762,
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1273	129	5.8	4374	45	US-10-128-572-2	Sequence 2, Appli
1274	129	5.8	4374	58	US-11-598-148-333	Sequence 333, App
1275	129	5.8	4374	31	US-60-836-986-524	Sequence 524, App
1276	129	5.8	4417	40	US-10-194-385-2	Sequence 2, Appli
1277	129	5.8	4417	40	US-11-041-102-22	Sequence 22, Appl
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1279	129	5.8	234	1	PCT-US06-61062-120	Sequence 120, App
1280	128.5	5.8	234	51	US-11-561-363-120	Sequence 120, App
1281	128.5	5.8	234	1	US-60-167-217-1033	Sequence 1033, Ap
1282	128.5	5.8	285	44	PCT-US07-62986-22	Sequence 22, Appl
1283	128.5	5.8	364	53	US-11-443-428A-797086	Sequence 797086,
1284	128.5	5.8	364	53	US-60-385-568-234	Sequence 234, App
1285	128.5	5.8	634	53	US-60-385-568-359	Sequence 359, App

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1292	128.5	5.8	770	US-11-443-428A-1026172	44	Sequence 1026172,
1293	128	5.8	249	PCT-US01-15624-20	1	Sequence 20, Appl
1294	128	5.8	249	US-08-928-361-20	19	Sequence 20, Appl
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1301	128	5.8	605	US-09-801-368-428	28	Sequence 428, App
1302	128	5.8	605	US-10-309-407-428	33	Sequence 428, App
1303	128	5.8	605	US-10-369-493-22016	33	Sequence 22016, A
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1305	128	5.8	870	US-10-326-956-1731	33	Sequence 1731, Ap
1306	128	5.8	1796	US-60-324-109-27892	53	Sequence 27892, A
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1311	127.5	5.8	424	US-10-366-965-421	43	Sequence 421, App
1312	127.5	5.8	529	US-11-443-428A-1026195	44	Sequence 1026195,
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1316	127.5	5.8	559	US-11-443-428A-895722	44	Sequence 895722,
1317	127.5	5.8	559	US-11-443-428A-895723	44	Sequence 895723,
1318	127.5	5.8	559	US-11-443-428A-895724	44	Sequence 895724,
1319	127.5	5.8	559	US-60-452-680-23607	54	Sequence 23607, A
1320	127.5	5.8	577	US-11-293-697-3929	42	Sequence 3929, Ap
1321	127.5	5.8	598	US-11-443-428A-1026193	44	Sequence 1026193,
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1327	127.5	5.8	821	US-11-443-428A-1026169	44	Sequence 1026169,
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     and is derived by analysis of the total score distribution.

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5	144	6.5	4295	7	US-11-490-374A-755	Sequence 755, App
6	143	5.6	404	7	US-11-374-300-26027	Sequence 26027, A
7	124.5	5.6	503	6	US-10-560-103-4	Sequence 4, Appli
8	123.5	5.6	165	7	US-11-374-300-5674	Sequence 5674, Ap
9	123	5.4	519	7	US-11-374-300-8977	Sequence 8977, Ap
10	119.5	5.3	768	7	US-11-374-300-10335	Sequence 10335, A
11	117.5	5.2	540	7	US-11-509-924-2	Sequence 2, Appli
12	116	5.2	954	7	US-11-374-300-47449	Sequence 47449, A
13	116	5.2	536	7	US-11-836-317-21	Sequence 21, Appl
14	115	5.2	555	7	US-11-836-317-15	Sequence 15, Appl
15	115	5.2	555	7	US-11-836-317-18	Sequence 18, Appl
16	114	5.2	507	7	US-11-374-300-38063	Sequence 38063, A
17	112.5	5.1	515	7	US-11-374-300-39353	Sequence 39353, A
18	112	5.1	967	1	PCT-US07-18368A-17590	Sequence 17590, A
19	112	5.1	967	7	US-11-374-300-16219	Sequence 16219, A
20	111.5	5.0	1090	7	US-11-374-300-2736	Sequence 2736, Ap
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22	110	5.0	310	7	US-11-781-665-4190	Sequence 4190, Ap
23	110	5.0	443	1	PCT-US07-18368A-9398	Sequence 9398, Ap
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33	106.5	4.8	1058	7	US-11-374-300-970	Sequence 970, App
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49	103	4.7	1117	7	US-11-490-374A-313	Sequence 313, App
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248	4.0	88.5	662	US-10-815-495A-6	6	Sequence 6, Appli
249	4.0	88.5	662	US-11-837-279-6	7	Sequence 6, Appli
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256	4.0	88.5	1347	US-11-374-300-10717	7	Sequence 10717, A
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258	4.0	88.5	1482	PCT-US07-18368A-29744	1	Sequence 29744, A
259	4.0	88	527	US-11-374-300-26783	7	Sequence 26783, A
260	4.0	88	557	US-11-374-300-39658	7	Sequence 39658, A
261	4.0	88	584	US-11-374-300-1405	7	Sequence 1405, Ap
262	4.0	88	621	US-11-374-300-36283	7	Sequence 36283, A
263	4.0	88	791	US-11-374-300-28451	7	Sequence 28451, A
264	4.0	88	811	US-11-816-601-210	7	Sequence 210, App
265	4.0	88	924	US-11-374-300-8970	7	Sequence 8970, Ap
266	4.0	88	1023	US-11-374-300-22424	7	Sequence 22424, A
267	4.0	88	1338	US-11-374-300-8129	7	Sequence 8129, Ap
268	4.0	88	1338	PCT-US07-18368A-9698	1	Sequence 9698, Ap
269	4.0	88	1338	PCT-US07-18368A-14230	1	Sequence 14230, A
270	4.0	88	1338	US-11-374-300-9375	7	Sequence 9375, Ap
271	4.0	88	1338	US-11-374-300-13336	7	Sequence 13336, A
272	4.0	87.5	1362	US-11-816-601-757	7	Sequence 757, App
273	4.0	87.5	1362	US-11-816-601-835	7	Sequence 835, APP
274	4.0	87.5	1478	PCT-US07-18368A-14314	1	Sequence 14314, A
275	4.0	87.5	1478	US-11-374-300-39174	7	Sequence 39174, A
276	4.0	87.5	282	US-11-374-300-1073	7	Sequence 1073, Ap
277	4.0	87.5	335	PCT-US07-18368A-8326	1	Sequence 8326, Ap
278	4.0	87.5	371	US-11-374-300-39868	7	Sequence 39868, A
279	4.0	87.5	422	PCT-US07-18368A-23086	1	Sequence 23086, A
280	4.0	87.5	461	PCT-US07-18368A-23073	1	Sequence 23073, A
281	4.0	87.5	461	PCT-US07-18368A-24333	1	Sequence 24333, A
282	4.0	87.5	467	US-11-374-300-39069	7	Sequence 39069, A
283	4.0	87.5	518	US-11-802-321A-67	7	Sequence 67, Appl
284	4.0	87.5	916	US-11-374-300-6872	7	Sequence 6872, Ap
285	4.0	87.5	971	US-11-374-300-31450	7	Sequence 31450, A
286	4.0	87.5	1628	PCT-US07-18368A-27969	1	Sequence 27969, A
287	3.9	87	2332	US-10-031-938D-4	6	Sequence 4, Appli
288	3.9	87	2799	PCT-US07-18368A-25053	1	Sequence 25053, A
289	3.9	87	294	US-11-374-300-34690	7	Sequence 34690, A
290	3.9	87	564	PCT-US07-18368A-525	1	Sequence 525, App
291	3.9	87	626	PCT-US07-18368A-4114	1	Sequence 4114, Ap
292	3.9	87	786	US-11-374-300-24004	7	Sequence 24004, A
293	3.9	87	869	US-11-374-300-20883	7	Sequence 20883, A
294	3.9	86.5	939	US-11-374-300-20919	7	Sequence 20919, A
295	3.9	86.5	939	US-11-374-300-20923	7	Sequence 20923, A
296	3.9	86.5	939	US-11-374-300-20923	7	Sequence 20923, A
297	3.9	86.5	1071	US-11-374-300-11026	7	Sequence 11026, A
298	3.9	86.5	1533	US-11-881-406-64	7	Sequence 64, Appl
299	3.9	86.5	2172	US-11-374-300-43547	7	Sequence 43547, A
300	3.9	86.5	271	US-11-801-963A-5266	7	Sequence 5266, Ap
301	3.9	86.5	290	US-11-374-300-16031	7	Sequence 16031, A
302	3.9	86.5	290	US-11-374-300-1034	7	Sequence 1034, Ap
303	3.9	86.5	627	US-11-374-300-19170	7	Sequence 19170, A
304	3.9	86.5	658	PCT-US07-18368A-17161	1	Sequence 17161, A
305	3.9	86.5	670	US-11-374-300-13138	7	Sequence 13138, A
306	3.9	86.5	701	US-11-374-300-41008	7	Sequence 41008, A
307	3.9	86.5	710	US-11-374-300-31393	7	Sequence 31393, A
308	3.9	86.5	742	US-11-374-300-24526	7	Sequence 24526, A
309	3.9	86.5	885	US-11-235-701A-232	7	Sequence 232, App
310	3.9	86.5	891	PCT-US07-18368A-27694	1	Sequence 27694, A
311	3.9	86.5	891	PCT-US07-18368A-14244	1	Sequence 14244, A

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318	3.9	86.5	891	US-11-374-300-39114	7	Sequence 39114, A
319	3.9	86.5	969	PCT-US07-18368A-1190	1	Sequence 1190, Ap
320	3.9	86.5	993	PCT-US07-18368A-1191	1	Sequence 1191, Ap
321	3.9	86.5	1029	US-11-374-300-19049	7	Sequence 19049, A
322	3.9	86.5	1136	US-11-374-300-7454	7	Sequence 7454, Ap
323	3.9	86.5	1207	US-11-374-300-23353	7	Sequence 23353, A
324	3.9	86.5	1207	US-11-374-300-39357	7	Sequence 39357, A
325	3.9	86.5	1574	PCT-US07-18368A-9029	1	Sequence 9029, A
326	3.9	86.5	1870	US-11-374-300-21537	7	Sequence 21537, A
327	3.9	86.5	1870	US-11-374-300-1336	7	Sequence 11336, A
328	3.9	86	334	PCT-US07-18368A-6036	1	Sequence 6036, Ap
329	3.9	86	381	US-11-825-627-300	7	Sequence 300, APP
330	3.9	86	474	PCT-US07-18368A-6813	1	Sequence 6813, Ap
331	3.9	86	527	US-11-374-300-41525	7	Sequence 41525, A
332	3.9	86	586	US-11-374-300-40896	7	Sequence 40896, A
333	3.9	86	621	PCT-US07-18368A-6478	1	Sequence 6478, Ap
334	3.9	86	628	US-11-374-300-20861	7	Sequence 20861, A
335	3.9	86	683	US-11-374-300-46072	7	Sequence 46072, A
336	3.9	86	683	US-11-374-300-45826	7	Sequence 45826, A
337	3.9	86	699	US-10-276-032-108	6	Sequence 108, App
338	3.9	86	901	US-11-374-300-25373	7	Sequence 25373, A
339	3.9	86	1168	US-11-374-300-7949	7	Sequence 7949, Ap
340	3.9	86	1276	US-11-374-300-12934	7	Sequence 12934, A
341	3.9	86	1283	US-11-374-300-20638	7	Sequence 20638, A
342	3.9	86	1340	US-11-374-300-39394	7	Sequence 39394, A
343	3.9	86	1551	PCT-US02-29555-4	1	Sequence 4, Appli
344	3.9	86	2468	US-11-832-579-19	7	Sequence 19, Appl
345	3.9	85.5	446	US-11-374-300-28433	7	Sequence 28433, A
346	3.9	85.5	684	US-11-374-300-31696	7	Sequence 31696, A
347	3.9	85.5	693	US-11-374-300-9634	7	Sequence 9634, Ap
348	3.9	85.5	748	US-11-374-300-29547	7	Sequence 29547, A
349	3.9	85.5	783	US-11-374-300-12374	7	Sequence 12374, A
350	3.9	85.5	800	US-11-374-300-35839	7	Sequence 35839, A
351	3.9	85.5	800	US-11-374-300-47496	7	Sequence 47496, A
352	3.9	85.5	868	US-11-374-300-37945	7	Sequence 37945, A
353	3.9	85.5	870	PCT-US07-18368A-23239	1	Sequence 23239, A
354	3.9	85.5	891	US-11-374-300-20903	7	Sequence 20903, A
355	3.8	85.5	891	US-11-374-300-46236	7	Sequence 46236, A
356	3.8	85.5	1359	US-11-374-300-47768	7	Sequence 47768, A
357	3.8	85.5	1651	US-11-490-374A-427	7	Sequence 427, App
358	3.8	85.5	1822	US-11-490-374A-429	7	Sequence 429, App
359	3.8	85.5	1822	US-11-490-374A-430	7	Sequence 430, App
360	3.8	85.5	1822	US-11-490-374A-434	7	Sequence 434, App
361	3.8	85.5	1822	US-11-883-996-18	7	Sequence 18, Appl
362	3.8	85	328	US-11-374-300-28361	7	Sequence 28361, A
363	3.8	85	407	US-11-374-300-43953	7	Sequence 43953, A
364	3.8	85	453	US-11-374-300-49216	7	Sequence 49216, A
365	3.8	85	672	US-11-374-300-40138	7	Sequence 40138, A
366	3.8	85	706	US-11-235-701A-231	7	Sequence 231, App
367	3.8	85	706	PCT-US07-18368A-6965	1	Sequence 6965, Ap
368	3.8	84.5	699	US-11-374-300-6925	7	Sequence 6925, Ap
369	3.8	84.5	700	US-11-665-940-32	7	Sequence 32, Appl
370	3.8	84.5	10203	US-11-374-300-9364	7	Sequence 9364, A
371	3.8	84.5	217	US-11-374-300-15268	7	Sequence 15268, A
372	3.8	84.5	385	US-11-374-300-48300	7	Sequence 48300, A
373	3.8	84.5	387	US-11-374-300-45279	7	Sequence 45279, A
374	3.8	84.5	561	US-11-374-300-43234	7	Sequence 43234, A
375	3.8	84.5	634	US-11-884-546-69	7	Sequence 69, Appl
376	3.8	84.5	640	US-11-374-300-40209	7	Sequence 40209, A
377	3.8	84.5	668	US-11-374-300-49216	7	Sequence 49216, A
378	3.8	84.5	672	US-11-374-300-40138	7	Sequence 40138, A
379	3.8	84.5	676	US-11-235-701A-228	7	Sequence 228, App
380	3.8	84.5	699	US-11-235-701A-229	7	Sequence 229, App
381	3.8	84.5	700	US-11-235-701A-226	7	Sequence 226, App
382	3.8	84.5	742	US-11-235-701A-240	7	Sequence 240, App
383	3.8	84.5	743	PCT-US07-18368A-7629	1	Sequence 7629, Ap
384	3.8	84.5	743	PCT-US07-18368A-7559	1	Sequence 7559, Ap
385	3.8	84.5	775	PCT-US07-18368A-4606	1	Sequence 4606, Ap
386	3.8	84	775	US-11-374-300-29016	7	Sequence 29016, A
387	3.8	84	979	PCT-US07-18368A-12412	1	Sequence 12412, A
388	3.8	84	979	US-11-374-300-24644	7	Sequence 24644, A
389	3.8	84	332	US-11-374-300-36202	7	Sequence 36202, A
390	3.8	84	522	PCT-US07-18368A-28291	1	Sequence 28291, A

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391	84	3.8	669	7	US-11-235-701A-234	Sequence 234, App
392	84	3.8	718	7	US-11-374-300-6871	Sequence 6871, Ap
393	84	3.8	733	7	US-11-490-374A-239	Sequence 239, App
394	84	3.8	733	7	US-11-490-374A-240	Sequence 240, App
395	84	3.8	733	7	US-11-490-374A-241	Sequence 241, App
396	84	3.8	927	1	PCT-US07-18368A-9980	Sequence 9980, A
397	84	3.8	1037	1	PCT-US07-18368A-26323	Sequence 26323, A
398	84	3.8	1037	1	PCT-US07-18368A-25049	Sequence 25049, A
399	84	3.8	1071	1	US-11-374-300-23705	Sequence 23705, A
400	84	3.8	1071	1	US-11-374-300-22579	Sequence 22579, A
401	84	3.8	2446	1	US-11-490-374A-283	Sequence 283, App
402	84	3.8	2477	7	US-11-490-374A-273	Sequence 273, App
403	84	3.8	2477	7	US-11-490-37A-280	Sequence 280, App
404	83.5	3.8	373	6	US-10-560-103-5	Sequence 5, Appli
405	83.5	3.8	390	7	US-11-374-300-36344	Sequence 36344, A
406	83.5	3.8	550	7	US-11-374-300-44590	Sequence 44590, A
407	83.5	3.8	553	7	US-11-374-300-42482	Sequence 42482, A
408	83.5	3.8	561	7	US-11-374-300-30042	Sequence 30042, A
409	83.5	3.8	561	7	US-11-374-300-36778	Sequence 36778, A
410	83.5	3.8	562	7	US-11-374-300-16619	Sequence 16619, A
411	83.5	3.8	581	7	US-11-825-627-98	Sequence 98, Appl
412	83.5	3.8	596	7	US-11-374-300-46091	Sequence 46091, A
413	83.5	3.8	596	7	US-11-374-300-49855	Sequence 49855, A
414	83.5	3.8	668	7	US-11-374-300-44853	Sequence 44853, A
415	83.5	3.8	695	7	US-11-374-300-42254	Sequence 42254, A
416	83.5	3.8	700	7	US-11-374-300-43062	Sequence 43062, A
417	83.5	3.8	822	7	US-11-374-300-32928	Sequence 32928, A
418	83.5	3.8	835	7	US-11-374-300-5250	Sequence 5250, Ap
419	83.5	3.8	1238	7	US-11-374-300-5591	Sequence 5591, Ap
420	83.5	3.8	1238	7	US-11-374-300-8996	Sequence 8996, Ap
421	83.5	3.8	1238	7	US-11-374-300-24842	Sequence 24842, A
422	83.5	3.8	1238	7	US-11-374-300-48166	Sequence 48166, A
423	83.5	3.8	1847	1	US-11-374-300-15620	Sequence 15620, A
424	83.5	3.8	1919	7	US-11-374-300-19214	Sequence 19214, A
425	83.5	3.8	2421	7	US-11-490-374A-270	Sequence 270, App
426	83.5	3.8	2421	7	US-11-490-374A-272	Sequence 272, App
427	83	3.8	346	8	US-60-970-876-56	Sequence 56, Appl
428	83	3.8	395	7	PCT-US07-18368A-1598	Sequence 1598, Ap
429	83	3.8	403	7	US-11-374-300-12161	Sequence 12161, A
430	83	3.8	426	7	PCT-US07-18368A-2843	Sequence 2843, Ap
431	83	3.8	446	7	US-11-374-300-32626	Sequence 32626, A
432	83	3.8	507	7	US-11-374-300-32602	Sequence 32602, A
433	83	3.8	552	7	PCT-US07-18368A-24429	Sequence 24429, A
434	83	3.8	559	1	US-11-374-300-13216	Sequence 13216, A
435	83	3.8	559	1	US-11-374-300-49806	Sequence 49806, A
436	83	3.8	608	7	US-11-374-300-7736	Sequence 7736, Ap
437	83	3.8	608	7	US-11-374-300-32362	Sequence 32362, A
438	83	3.8	636	7	US-11-374-300-2813	Sequence 2813, Ap
439	83	3.8	873	7	US-11-374-300-37366	Sequence 37366, A
440	83	3.8	886	7	US-11-374-300-49084	Sequence 49084, A
441	83	3.8	1068	1	PCT-US07-18368A-13085	Sequence 13085, A
442	82.5	3.8	3896	7	US-11-374-300-12173	Sequence 12173, A
443	82.5	3.8	270	7	US-11-883-996-75	Sequence 75, Appl
444	82.5	3.8	350	1	PCT-US07-18368A-10316	Sequence 10316, A
445	82.5	3.8	492	1	PCT-US07-18368A-9874	Sequence 9874, Ap
446	82.5	3.7	545	1	PCT-US07-18368A-12980	Sequence 12980, A
447	82.5	3.7	559	1	US-11-374-300-16711	Sequence 16711, A
448	82.5	3.7	811	7	PCT-US07-18368A-16571	Sequence 16571, A
449	82.5	3.7	873	7	US-11-374-300-12075	Sequence 12075, A
450	82.5	3.7	925	7	US-11-374-300-25051	Sequence 25051, A
451	82.5	3.7	987	7	US-11-374-300-19786	Sequence 19786, A
452	82.5	3.7	1224	7	PCT-US07-18368A-4660	Sequence 4660, Ap
453	82.5	3.7	1364	1	US-11-374-300-47395	Sequence 47395, A
454	82.5	3.7	7257	1	US-11-374-300-34856	Sequence 34856, A
455	82	3.7	414	7	US-11-490-374A-244	Sequence 244, App
456	82	3.7	418	7	PCT-US07-18368A-16024	Sequence 16024, A
457	82	3.7	569	1	PCT-US07-18368A-23852	Sequence 23852, A
458	82	3.7	647	7	US-11-374-300-40451	Sequence 40451, A
459	82	3.7	693	7	US-11-374-300-9538	Sequence 9538, Ap
460	82	3.7	779	1	PCT-US07-18368A-8832	Sequence 8832, Ap
461	82	3.7	817	7	US-11-374-300-29227	Sequence 29227, A
462	82	3.7	817	7	US-11-374-300-22611	Sequence 22611, A
463	82	3.7	822	7	US-11-374-300-22611	Sequence 22611, A
464	82	3.7	1633	1	PCT-US07-18368A-18647	Sequence 18647, A
465	82	3.7	1764	1	PCT-US07-18368A-26691	Sequence 26691, A
466	82	3.7	1764	1	US-11-374-300-49497	Sequence 49497, A
467	82	3.7	1902	7	US-11-825-627-321	Sequence 321, App
468	82	3.7	1914	7	US-11-374-300-45371	Sequence 45371, A
469	81.5	3.7	394	7	US-11-374-300-10575	Sequence 10575, A
470	81.5	3.7	441	7	US-11-374-300-26432	Sequence 26432, A
471	81.5	3.7	443	7	US-11-374-300-11276	Sequence 11276, A
472	81.5	3.7	468	7	PCT-US07-18368A-26733	Sequence 26733, A
473	81.5	3.7	492	7	PCT-US07-18368A-10350	Sequence 10350, A
474	81.5	3.7	516	7	US-11-374-300-4645	Sequence 4645, Ap
475	81.5	3.7	532	7	PCT-US07-18368A-8293	Sequence 8293, Ap
476	81.5	3.7	692	7	US-11-908-114-35	Sequence 35, Appl
477	81.5	3.7	774	7	US-11-374-300-16222	Sequence 16222, A
478	81.5	3.7	798	7	US-11-374-300-29444	Sequence 29444, A
479	81.5	3.7	805	7	US-11-374-300-21352	Sequence 21352, A
480	81.5	3.7	808	7	US-11-374-300-20391	Sequence 20391, A
481	81.5	3.7	871	7	PCT-US07-18368A-20829	Sequence 20829, A
482	81.5	3.7	928	1	PCT-US07-18368A-6779	Sequence 6779, Ap
483	81.5	3.7	946	1	PCT-US07-18368A-16326	Sequence 16326, A
484	81.5	3.7	1120	7	US-11-374-300-16537	Sequence 16537, A
485	81.5	3.7	1302	7	US-11-374-300-24340	Sequence 24340, A
486	81.5	3.7	1518	7	PCT-US07-18368A-30282	Sequence 30282, A
487	81.5	3.7	1518	7	US-11-374-300-27391	Sequence 27391, A
488	81.5	3.7	2544	7	US-11-374-300-16996	Sequence 16996, A
489	81.5	3.7	7257	1	US-11-374-300-44001	Sequence 44001, A
490	81	3.7	196	7	US-11-374-300-42661	Sequence 42661, A
491	81	3.7	235	7	US-11-665-940-29	Sequence 29, Appl
492	81	3.7	275	7	US-11-781-818-62	Sequence 62, Appl
493	81	3.7	399	7	US-11-374-300-6866	Sequence 6866, Ap
494	81	3.7	399	7	US-11-374-300-8263	Sequence 8263, Ap
495	81	3.7	399	7	US-11-374-300-16233	Sequence 16233, A
496	81	3.7	410	7	US-11-490-374A-389	Sequence 389, App
497	81	3.7	410	7	US-11-490-374A-392	Sequence 392, App
498	81	3.7	478	7	PCT-US07-18368A-9609	Sequence 9609, Ap
499	81	3.7	481	7	US-11-374-300-45877	Sequence 45877, A
500	81	3.7	492	7	PCT-US07-18368A-10318	Sequence 10318, A
501	81	3.7	646	7	PCT-US07-18368A-8988	Sequence 8988, Ap
502	81	3.7	682	7	US-11-374-300-24827	Sequence 24827, A
503	81	3.7	698	7	US-11-374-300-19725	Sequence 19725, A
504	81	3.7	698	7	US-11-374-300-42041	Sequence 42041, A
505	81	3.7	760	7	PCT-US07-18368A-23849	Sequence 23849, A
506	81	3.7	790	7	PCT-US07-18368A-12920	Sequence 12920, A
507	81	3.7	799	7	PCT-US07-18368A-3608	Sequence 3608, Ap
508	81	3.7	800	7	PCT-US07-18368A-17020	Sequence 17020, A
509	81	3.7	917	7	PCT-US07-18368A-13576	Sequence 13576, A
510	81	3.7	917	7	US-11-374-300-22139	Sequence 22139, A
511	81	3.7	933	7	PCT-US07-18368A-28900	Sequence 28900, A
512	81	3.7	1033	7	US-11-374-300-44149	Sequence 44149, A
513	81	3.7	1103	7	PCT-US07-18368A-8791	Sequence 8791, Ap
514	81	3.7	1103	7	US-11-374-300-8564	Sequence 8564, Ap
515	81	3.7	1142	1	PCT-US07-18368A-22566	Sequence 22566, A
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519	81	3.7	1176	1	PCT-US07-18368A-16060	Sequence 16060, A
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521	81	3.7	1733	1	PCT-US07-18368A-28256	Sequence 28256, A
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523	80.5	3.6	426	7	US-11-374-300-41225	Sequence 41225, A
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525	80.5	3.6	518	7	PCT-US07-13803-552	Sequence 552, App
526	80.5	3.6	518	7	PCT-US07-13803-792	Sequence 792, App
527	80.5	3.6	558	7	US-11-374-300-49009	Sequence 49009, A
528	80.5	3.6	559	1	PCT-US07-13803-736	Sequence 736, App
529	80.5	3.6	559	1	PCT-US07-13803-793	Sequence 793, App
530	80.5	3.6	616	7	PCT-US07-18368A-17712	Sequence 17712, A
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534	80.5	3.6	676	7	US-11-374-300-9697	Sequence 9697, Ap
535	80.5	3.6	713	7	US-11-374-300-15016	Sequence 15016, A
536	80.5	3.6	743	7	US-11-374-300-21663	Sequence 21663, A

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542	80.5	3.6	1273	7	US-11-374-300-35873	Sequence 35873, A
543	80.5	3.6	2072	7	US-11-374-300-35793	Sequence 35793, A
544	80	3.6	216	1	PCT-US07-18368A-12054	Sequence 12054, A
545	80	3.6	216	7	US-11-374-300-11415	Sequence 11415, A
546	80	3.6	335	7	US-11-374-300-553	Sequence 553, App
547	80	3.6	379	1	PCT-US07-18368A-2680	Sequence 2680, App
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565	80	3.6	1875	7	US-11-490-374A-433	Sequence 433, App
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570	79.5	3.6	360	7	US-11-831-404-135	Sequence 135, App
571	79.5	3.6	410	7	US-11-490-374A-391	Sequence 391, App
572	79.5	3.6	410	7	US-11-490-374A-393	Sequence 393, App
573	79.5	3.6	428	1	PCT-US07-18368A-21288	Sequence 21288, A
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575	79.5	3.6	486	7	US-11-816-233-139	Sequence 139, Appl
576	79.5	3.6	500	7	US-11-825-627-7	Sequence 7, Appli
577	79.5	3.6	526	7	US-11-374-300-32386	Sequence 32386, A
578	79.5	3.6	560	7	US-11-374-300-18946	Sequence 18946, A
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588	79.5	3.6	894	7	US-11-374-300-31780	Sequence 31780, A
589	79.5	3.6	917	7	US-11-374-300-6814	Sequence 6814, Ap
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603	79	3.6	441	7	US-11-816-233-138	Sequence 138, Appl
604	79	3.6	502	7	US-11-374-300-33814	Sequence 33814, A
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617	79	3.6	914	7	US-11-374-300-13001	Sequence 13001, A
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627	78.5	3.6	2101	7	US-11-490-374A-32	Sequence 32, Appl
628	78.5	3.6	2110	7	US-11-490-374A-34	Sequence 34, Appl
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630	78.5	3.6	2115	7	US-11-490-374A-36	Sequence 36, Appl
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633	78.5	3.6	365	1	US-11-188-807A-28	Sequence 28, Appl
634	78.5	3.6	434	1	US-11-816-601-215	Sequence 215, App
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638	78.5	3.6	529	1	US-11-374-300-4389	Sequence 4389, Ap
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646	78.5	3.6	658	7	US-11-374-300-23831	Sequence 23831, A
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707	77.5	3.5	479	7	US-11-374-300-25408	Sequence 25408, A
708	77.5	3.5	486	7	US-11-816-233-150	Sequence 150, App
709	77.5	3.5	512	7	US-11-374-300-30357	Sequence 30357, A
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711	77.5	3.5	561	7	US-11-374-300-29416	Sequence 29416, A
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713	77.5	3.5	570	7	US-11-374-300-17179	Sequence 17179, A
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14	115	5.2	555	7	US-11-836-317-15	Sequence 15, Appl
15	115	5.2	555	7	US-11-836-317-18	Sequence 18, Appl
16	114	5.2	507	7	US-11-374-300-38063	Sequence 38063, A
17	112.5	5.1	515	7	US-11-374-300-39353	Sequence 39353, A
18	112	5.1	967	1	PCT-US07-18368A-17590	Sequence 17590, A
19	112	5.1	967	7	US-11-374-300-16219	Sequence 16219, A
20	111.5	5.0	1090	7	US-11-374-300-2736	Sequence 2736, Ap
21	111	5.0	349	1	PCT-US07-18368A-22211	Sequence 22211, A
22	110	5.0	310	7	US-11-781-665-4190	Sequence 4190, Ap
23	110	5.0	443	1	PCT-US07-18368A-9398	Sequence 9398, Ap
24	110	5.0	466	7	US-11-374-300-36878	Sequence 36878, A
25	109.5	5.0	1749	1	PCT-US07-18368A-3106	Sequence 3106, Ap
26	109.5	5.0	1749	7	US-11-374-300-29482	Sequence 29482, A
27	109	4.9	1436	7	US-11-374-300-30868	Sequence 30868, A
28	108.5	4.9	637	7	US-11-817-472-25	Sequence 25, Appl
29	108.5	4.9	727	7	US-11-374-300-34563	Sequence 34563, A
30	108	4.9	661	1	PCT-US07-76717-23	Sequence 23, Appl
31	107.5	4.9	911	7	US-11-374-300-22703	Sequence 22703, A
32	107.5	4.9	1058	1	PCT-US07-18368A-1937	Sequence 1937, Ap
33	106.5	4.8	1058	7	US-11-374-300-2567	Sequence 2567, Ap
34	106.5	4.8	512	7	US-11-490-374A-970	Sequence 970, App
35	106.5	4.8	1099	7	US-11-374-300-18502	Sequence 18502, A
36	106	4.8	1686	7	US-11-815-821-1	Sequence 1, Appli
37	106	4.8	728	7	US-11-374-300-37129	Sequence 37129, A
38	106	4.8	762	7	US-11-374-300-4566	Sequence 4566, Ap
39	105.5	4.8	1979	7	US-11-374-300-37391	Sequence 37391, A
40	105.5	4.8	645	7	US-11-817-472-24	Sequence 24, Appl
41	104	4.7	1069	7	US-11-374-300-3286	Sequence 3286, Ap
42	104	4.7	310	7	US-11-781-665-5485	Sequence 5485, Ap
43	104	4.7	452	7	US-11-374-300-46306	Sequence 46306, A
44	103	4.7	714	7	US-11-572-719-24	Sequence 24, Appl
45	103	4.7	447	7	US-11-832-579-3	Sequence 3, Appli
46	103	4.7	447	7	US-11-572-719-6	Sequence 6, Appli
47	103	4.7	447	7	US-11-832-579-13	Sequence 13, Appl
48	103	4.7	955	7	US-11-354-210-103	Sequence 103, App
49	103	4.7	1117	7	US-11-816-601-338	Sequence 338, App
50	103	4.7	1117	7	US-11-490-374A-313	Sequence 313, App
51	102.5	4.6	1118	7	US-11-490-374A-314	Sequence 314, App
52	102.5	4.6	391	7	US-11-374-300-4110	Sequence 4110, Ap
53	102.5	4.6	597	7	US-11-374-300-23608	Sequence 23608, A
54	102.5	4.6	640	7	US-11-795-915-334	Sequence 334, App
55	102.5	4.6	663	7	US-11-817-472-20	Sequence 20, Appl
56	102.5	4.6	694	7	US-11-374-300-27488	Sequence 27488, A
57	102.5	4.6	717	7	US-11-374-300-46589	Sequence 46589, A
58	102.5	4.6	1362	7	US-11-374-300-42402	Sequence 42402, A
59	102.5	4.6	1362	1	PCT-US07-18368A-16893	Sequence 16893, A
60	102	4.6	652	7	US-11-374-300-15596	Sequence 15596, A
61	102	4.6	652	7	US-11-374-300-5066	Sequence 5066, Ap
62	102	4.6	1284	7	US-11-374-300-41982	Sequence 41982, A
63	102	4.6	1576	7	US-11-374-300-42942	Sequence 42942, A
64	102	4.6	512	1	PCT-US07-18368A-27838	Sequence 27838, A
65	101.5	4.6	648	7	US-11-490-374A-971	Sequence 971, App
66	101.5	4.6	422	7	US-11-817-472-21	Sequence 21, Appl
67	101	4.6	422	7	US-11-235-701A-89	Sequence 89, Appl
68	101	4.6	533	7	US-11-490-374A-769	Sequence 769, App
69	101	4.6	533	7	US-11-235-701A-102	Sequence 102, App
70	101	4.6	672	7	US-11-490-374A-782	Sequence 782, App
71	101	4.6	1288	7	US-11-374-300-27554	Sequence 27554, A
72	101	4.6	625	7	US-11-374-300-42232	Sequence 42232, A
73	100.5	4.5	625	7	US-11-374-300-6257	Sequence 6257, Ap
74	100.5	4.5	807	7	US-11-374-300-6425	Sequence 6425, Ap
75	100.5	4.5	478	1	PCT-US07-18368A-19942	Sequence 19942, A
76	100	4.5	2415	5	US-09-445-289G-34	Sequence 34, Appl
77	100	4.5	339	7	US-11-814-936-2	Sequence 2, Appli
78	99.5	4.5	597	7	US-11-374-300-46411	Sequence 46411, A
79	99.5	4.5	597	7	US-11-374-300-9412	Sequence 9412, Ap
80	99.5	4.5	915	7	US-11-374-300-46706	Sequence 46706, A
81	99.5	4.5	845	7	US-11-374-300-38028	Sequence 38028, A
82	99	4.5	1184	7	US-11-490-374A-179	Sequence 179, App
83	98.5	4.5	1184	7	US-11-374-300-6925	Sequence 6925, Ap
84	98.5	4.5	1192	7	US-11-374-300-6902	Sequence 6902, Ap
85	98.5	4.5	1192	1	PCT-US07-18368A-25048	Sequence 25048, A
86	98	4.4	419	7	US-11-374-300-22577	Sequence 22577, A
87	98	4.4	419	7	US-11-235-701A-100	Sequence 100, App
88	98	4.4	530	7	US-11-235-701A-780	Sequence 780, App
89	98	4.4	530	7	US-11-235-701A-94	Sequence 94, Appl
90	98	4.4	989	7	US-11-490-374A-774	Sequence 774, App
91	98	4.4	989	1	PCT-US07-18368A-21992	Sequence 21992, A
92	97.5	4.4	998	1	PCT-US07-18368A-26046	Sequence 26046, A
93	97.5	4.4	598	7	US-11-374-300-649	Sequence 649, App
94	97.5	4.4	944	1	PCT-US07-18368A-24439	Sequence 24439, A
95	97.5	4.4	1142	1	PCT-US07-18368A-18396	Sequence 18396, A
96	97.5	4.4	1458	7	US-11-569-756-7	Sequence 7, Appli
97	97.5	4.4	1842	6	US-10-741-191B-17	Sequence 17, Appl

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99	4.4	97	1667	US-11-374-300-15782	7	Sequence 15782, A
100	4.3	96	511	US-11-490-374A-972	7	Sequence 972, App
101	4.3	96	3729	US-11-374-300-24966	7	Sequence 24966, A
102	4.3	96	5541	US-11-374-300-3321	7	Sequence 3321, Ap
103	4.3	95.5	370	US-11-801-963A-4781	7	Sequence 4781, Ap
104	4.3	95.5	493	US-11-235-701A-242	7	Sequence 242, App
105	4.3	95.5	494	US-11-235-701A-233	7	Sequence 233, App
106	4.3	95.5	494	US-11-235-701A-241	7	Sequence 241, App
107	4.3	95.5	546	US-11-374-300-27969	7	Sequence 27969, A
108	4.3	95.5	643	US-11-374-300-1643	7	Sequence 1643, Ap
109	4.3	95.5	931	PCT-US07-13803-664	1	Sequence 664, App
110	4.3	95	382	US-10-498-694-2	6	Sequence 2, Appli
111	4.3	95	395	US-11-374-300-20613	7	Sequence 20613, A
112	4.3	95	570	US-11-490-374A-178	7	Sequence 178, App
113	4.3	95	605	US-10-560-103-2	6	Sequence 2, Appli
114	4.3	95	670	US-11-374-300-16052	7	Sequence 16052, A
115	4.3	95	679	US-11-490-374A-175	7	Sequence 175, App
116	4.3	95	702	US-11-374-300-36046	7	Sequence 36046, A
117	4.3	95	845	US-11-490-374A-176	7	Sequence 176, App
118	4.3	95	1230	US-11-374-300-30467	7	Sequence 30467, A
119	4.3	95	1230	US-11-374-300-35643	7	Sequence 35643, A
120	4.3	95	1412	US-11-374-300-22512	7	Sequence 22512, A
121	4.3	95	2349	US-11-782-310-68	7	Sequence 68, Appl
122	4.3	94.5	507	US-11-374-300-22921	7	Sequence 22921, A
123	4.3	94.5	533	US-11-374-300-21538	7	Sequence 21538, A
124	4.3	94.5	574	PCT-US07-18368A-13713	1	Sequence 13713, A
125	4.3	94.5	587	PCT-US07-18368A-24629	1	Sequence 24629, A
126	4.3	94.5	645	US-11-374-300-16131	7	Sequence 16131, A
127	4.3	94.5	645	US-11-374-300-44944	7	Sequence 44944, A
128	4.3	94.5	711	US-11-374-300-33956	7	Sequence 33956, A
129	4.3	94.5	1070	US-11-782-310-2166	7	Sequence 2166, Ap
130	4.3	94.5	1154	US-11-374-300-32965	7	Sequence 32965, A
131	4.3	94.5	1455	US-11-569-756-1	7	Sequence 1, Appli
132	4.3	94.5	1484	US-11-569-756-3	7	Sequence 3, Appli
133	4.3	94.5	1487	US-11-569-756-9	7	Sequence 9, Appli
134	4.3	94.5	1531	US-11-569-756-5	7	Sequence 5, Appli
135	4.3	94.5	1598	US-11-884-546-91	7	Sequence 91, Appl
136	4.3	94	517	US-11-374-300-37324	7	Sequence 37324, A
137	4.3	94	517	PCT-US07-18368A-22020	1	Sequence 22020, A
138	4.3	94	567	US-11-374-300-30205	7	Sequence 30205, A
139	4.3	94	999	US-60-970-281-43	8	Sequence 43, Appl
140	4.3	94	1542	US-11-374-300-8812	7	Sequence 8812, Ap
141	4.3	94	2176	US-11-490-374A-271	7	Sequence 271, App
142	4.3	94	2176	US-11-490-374A-294	7	Sequence 294, App
143	4.3	94	2296	US-11-490-374A-288	7	Sequence 288, App
144	4.3	94	2296	US-11-490-374A-289	7	Sequence 289, App
145	4.3	94	2330	US-11-490-374A-277	7	Sequence 277, App
146	4.3	94	2330	US-11-490-374A-284	7	Sequence 284, App
147	4.3	94	2355	US-11-490-374A-281	7	Sequence 281, App
148	4.3	94	2355	US-11-490-374A-291	7	Sequence 291, App
149	4.3	94	2355	US-11-490-374A-275	7	Sequence 275, App
150	4.3	94	2386	US-11-490-374A-290	7	Sequence 290, App
151	4.3	93.5	647	PCT-US07-18368A-29458	1	Sequence 29458, A
152	4.2	93.5	664	PCT-US07-18368A-2403	1	Sequence 2403, Ap
153	4.2	93.5	1541	PCT-US07-18368A-13534	1	Sequence 13534, A
154	4.2	93.5	2783	US-11-846-177-14	7	Sequence 14, Appl
155	4.2	93.5	2971	US-11-490-374A-1175	7	Sequence 1175, Ap
156	4.2	93.5	2976	US-11-490-374A-1173	7	Sequence 1173, Ap
157	4.2	93.5	2977	US-11-490-374A-1172	7	Sequence 1172, Ap
158	4.2	93.5	3010	US-11-374-300-804	7	Sequence 804, App
159	4.2	93.5	3177	US-11-490-374A-1176	7	Sequence 1176, Ap
160	4.2	93.5	463	US-11-272-833C-4	7	Sequence 4, Appli
161	4.2	93	482	US-11-374-300-8452	7	Sequence 8452, Ap
162	4.2	93	507	US-11-235-701A-91	7	Sequence 91, Appl
163	4.2	93	507	US-11-490-374A-771	7	Sequence 771, App
164	4.2	93	819	US-11-374-300-15929	7	Sequence 15929, A
165	4.2	93	863	PCT-US07-18368A-12119	1	Sequence 12119, A
166	4.2	93	863	US-11-374-300-11467	7	Sequence 11467, A
167	4.2	93	994	US-11-815-559-6	7	Sequence 6, Appli
168	4.2	93	994	PCT-US07-18368B-25643	1	Sequence 25643, A
169	4.2	93	1100	PCT-US07-18368A-26484	1	Sequence 26484, A
170	4.2	93	1478			
171	4.2	93	1478			

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No.	%	Score	Len	Accession	N	Sequence
172	93	4.2	1478	US-11-374-300-23140	7	Sequence 23140, A
173	93	4.2	1478	US-11-374-300-39459	7	Sequence 39459, A
174	93	4.2	2314	US-11-733-861-110	7	Sequence 110, App
175	92.5	4.2	404	US-10-343-663B-19	6	Sequence 19, Appl
176	92.5	4.2	404	US-10-343-663B-52	6	Sequence 52, Appl
177	92.5	4.2	408	US-11-374-300-20823	7	Sequence 20823, A
178	92.5	4.2	409	US-11-374-300-13621	7	Sequence 13621, A
179	92.5	4.2	645	US-11-374-300-46719	7	Sequence 46719, A
180	92.5	4.2	2019	US-11-781-861-4	7	Sequence 4, Appli
181	92.5	4.2	2019	US-11-781-867-4	7	Sequence 4, Appli
182	92.5	4.2	2019	US-11-781-870-4	7	Sequence 4, Appli
183	92.5	4.2	2019	US-11-781-871-4	7	Sequence 4, Appli
184	92.5	4.2	2019	US-11-781-874-4	7	Sequence 4, Appli
185	92.5	4.2	2019	US-11-781-875-4	7	Sequence 4, Appli
186	92.5	4.2	2019	US-11-781-877-4	7	Sequence 4, Appli
187	92.5	4.2	2019	US-11-781-880-4	7	Sequence 4, Appli
188	92	4.2	2019	US-11-781-882-4	7	Sequence 4, Appli
189	92	4.2	417	PCT-US07-18368A-10144	1	Sequence 10144, A
190	92	4.2	489	PCT-US07-18368A-4505	1	Sequence 4505, Ap
191	92	4.2	1034	PCT-US07-18368A-22352	1	Sequence 22352, A
192	92	4.2	1613	PCT-US07-18368A-8048	1	Sequence 8048, Ap
193	91.5	4.1	145	US-11-374-300-6611	7	Sequence 6611, Ap
194	91.5	4.1	147	US-11-374-300-11253	7	Sequence 11253, A
195	91.5	4.1	634	US-11-374-300-18255	7	Sequence 18255, A
196	91.5	4.1	1542	PCT-US07-18368A-21287	1	Sequence 21287, A
197	91	4.1	175	US-11-374-300-7462	7	Sequence 7462, Ap
198	91	4.1	656	US-11-374-300-42512	7	Sequence 42512, A
199	91	4.1	673	US-11-374-300-23979	7	Sequence 23979, A
200	91	4.1	706	US-11-374-300-47927	7	Sequence 47927, A
201	91	4.1	763	US-11-374-300-46951	7	Sequence 46951, A
202	91	4.1	1013	US-11-374-300-37920	7	Sequence 37920, A
203	91	4.1	1510	US-11-374-300-17828	7	Sequence 17828, A
204	91	4.1	3396	PCT-US07-13803-567	1	Sequence 567, App
205	90.5	4.1	408	US-11-374-300-20824	7	Sequence 20824, A
206	90.5	4.1	422	US-11-374-300-38946	7	Sequence 38946, A
207	90.5	4.1	446	US-11-832-579-9	7	Sequence 9, Appli
208	90.5	4.1	446	US-11-832-579-26	7	Sequence 26, Appl
209	90.5	4.1	446	US-11-832-579-32	7	Sequence 32, Appl
210	90.5	4.1	528	US-10-103-3	6	Sequence 3, Appli
211	90.5	4.1	528	US-11-802-321A-65	7	Sequence 65, Appl
212	90.5	4.1	528	US-11-490-374A-886	7	Sequence 886, App
213	90.5	4.1	574	PCT-US07-18368A-27377	1	Sequence 27377, A
214	90.5	4.1	753	US-11-816-601-230	7	Sequence 230, App
215	90	4.1	860	US-11-374-300-22538	7	Sequence 22538, A
216	90	4.1	381	US-11-825-627-302	7	Sequence 302, App
217	90	4.1	581	US-11-665-276-5	7	Sequence 5, Appli
218	90	4.1	686	US-11-374-300-33337	7	Sequence 33337, A
219	90	4.1	808	PCT-US07-18368A-20063	1	Sequence 20063, A
220	90	4.1	921	US-11-374-300-22422	7	Sequence 22422, A
221	90	4.1	1023	US-11-814-954-4	7	Sequence 4, Appli
222	90	4.1	1228	US-11-816-601-843	7	Sequence 843, App
223	89.5	4.0	396	US-11-816-601-756	7	Sequence 756, App
224	89.5	4.0	396	US-11-832-579-16	7	Sequence 16, Appl
225	89.5	4.0	446	US-11-832-579-22	7	Sequence 22, Appl
226	89.5	4.0	446	US-11-832-579-30	7	Sequence 30, Appl
227	89.5	4.0	612	US-11-374-300-31054	7	Sequence 31054, A
228	89.5	4.0	649	PCT-US07-18368A-27519	1	Sequence 27519, A
229	89.5	4.0	649	US-11-374-300-24821	7	Sequence 24821, A
230	89.5	4.0	708	US-11-374-300-12478	7	Sequence 12478, A
231	89.5	4.0	779	US-11-374-300-33855	7	Sequence 33855, A
232	89.5	4.0	793	US-11-374-300-13801	7	Sequence 13801, A
233	89.5	4.0	464	US-11-374-300-28293	7	Sequence 28293, A
234	89	4.0	490	US-11-374-300-25635	7	Sequence 25635, A
235	89	4.0	643	US-11-374-300-44557	7	Sequence 44557, A
236	89	4.0	686	US-11-374-300-6252	7	Sequence 6252, Ap
237	89	4.0	736	US-11-374-300-13483	7	Sequence 13483, A
238	89	4.0	921	PCT-US07-18368A-3627	1	Sequence 3627, Ap
239	89	4.0	921	US-11-374-300-29986	7	Sequence 29986, A
240	89	4.0	935	PCT-US07-18368A-21946	1	Sequence 21946, A
241	89	4.0	989	PCT-US07-18368A-23206	1	Sequence 23206, A
242	89	4.0	1512	PCT-US07-18368A-1151	1	Sequence 1151, Ap
243	89	4.0	2900	US-11-374-300-42957	7	Sequence 42957, A

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245	88.5	4.0	149	7	US-11-374-300-9244	Sequence 9244, Ap
246	88.5	4.0	351	7	US-11-800-955-18	Sequence 18, Appl
247	88.5	4.0	584	7	US-11-374-300-36160	Sequence 36160, A
248	88.5	4.0	662	6	US-10-815-495A-6	Sequence 6, Appli
249	88.5	4.0	662	7	US-11-837-279-6	Sequence 6, Appli
250	88.5	4.0	675	7	US-11-374-300-4153	Sequence 4153, Ap
251	88.5	4.0	704	6	US-10-587-995-3	Sequence 3, Appli
252	88.5	4.0	707	7	US-11-374-300-23343	Sequence 23343, A
253	88.5	4.0	756	1	PCT-US07-18368A-10069	Sequence 10069, A
254	88.5	4.0	1008	7	US-11-374-300-8765	Sequence 8765, Ap
255	88.5	4.0	1243	1	PCT-US07-13803-665	Sequence 665, App
256	88.5	4.0	1347	7	US-11-374-300-10717	Sequence 10717, A
257	88.5	4.0	1482	1	PCT-US07-18368A-29744	Sequence 29744, A
258	88.5	4.0	1482	7	US-11-374-300-26783	Sequence 26783, A
259	88	4.0	527	7	US-11-374-300-39658	Sequence 39658, A
260	88	4.0	557	7	US-11-374-300-1405	Sequence 1405, Ap
261	88	4.0	584	7	US-11-374-300-36283	Sequence 36283, A
262	88	4.0	621	7	US-11-374-300-28451	Sequence 28451, A
263	88	4.0	791	7	US-11-816-601-210	Sequence 210, App
264	88	4.0	811	7	US-11-374-300-8970	Sequence 8970, Ap
265	88	4.0	924	7	US-11-374-300-22424	Sequence 22424, A
266	88	4.0	1023	7	US-11-374-300-8129	Sequence 8129, Ap
267	88	4.0	1338	1	PCT-US07-18368A-9698	Sequence 9698, Ap
268	88	4.0	1338	1	PCT-US07-18368A-14230	Sequence 14230, A
269	88	4.0	1338	7	US-11-374-300-9375	Sequence 9375, Ap
270	88	4.0	1338	7	US-11-374-300-13336	Sequence 13336, A
271	88	4.0	1362	7	US-11-816-601-757	Sequence 757, App
272	88	4.0	1362	7	US-11-816-601-835	Sequence 835, App
273	88	4.0	1478	1	PCT-US07-18368A-14314	Sequence 14314, A
274	88	4.0	1478	1	PCT-US07-18368A-39174	Sequence 39174, A
275	87.5	4.0	282	7	US-11-374-300-1073	Sequence 1073, Ap
276	87.5	4.0	335	1	PCT-US07-18368A-8326	Sequence 8326, Ap
277	87.5	4.0	371	7	US-11-374-300-39868	Sequence 39868, A
278	87.5	4.0	422	1	PCT-US07-18368A-23086	Sequence 23086, A
279	87.5	4.0	461	1	PCT-US07-18368A-23073	Sequence 23073, A
280	87.5	4.0	461	1	PCT-US07-18368A-24333	Sequence 24333, A
281	87.5	4.0	467	7	US-11-374-300-39069	Sequence 39069, A
282	87.5	4.0	518	7	US-11-802-321A-67	Sequence 67, Appl
283	87.5	4.0	916	7	US-11-374-300-6872	Sequence 6872, Ap
284	87.5	4.0	971	7	US-11-374-300-31450	Sequence 31450, A
285	87.5	4.0	1628	1	PCT-US07-18368A-27969	Sequence 27969, A
286	87.5	4.0	2332	6	US-10-031-938D-4	Sequence 4, Appli
287	87.5	4.0	2799	1	PCT-US07-18368A-25053	Sequence 25053, A
288	87	3.9	294	7	US-11-374-300-34690	Sequence 34690, A
289	87	3.9	564	1	PCT-US07-18368A-525	Sequence 525, App
290	87	3.9	626	1	PCT-US07-18368A-4114	Sequence 4114, Ap
291	87	3.9	786	7	US-11-374-300-24004	Sequence 24004, A
292	87	3.9	869	7	US-11-881-406-45	Sequence 45, Appl
293	87	3.9	939	7	US-11-374-300-748	Sequence 748, App
294	86.5	3.9	939	7	US-11-374-300-11026	Sequence 11026, A
295	86.5	3.9	1071	7	US-11-802-321A-64	Sequence 64, Appl
296	86.5	3.9	1533	7	US-11-374-300-43547	Sequence 43547, A
297	86.5	3.9	2172	7	US-11-801-963A-5266	Sequence 5266, Ap
298	86.5	3.9	271	7	US-11-374-300-16031	Sequence 16031, A
299	86.5	3.9	290	7	US-11-374-300-1034	Sequence 1034, Ap
300	86.5	3.9	290	7	US-11-374-300-12751	Sequence 12751, A
301	86.5	3.9	408	7	US-11-374-300-20766	Sequence 20766, A
302	86.5	3.9	408	7	US-11-374-300-20883	Sequence 20883, A
303	86.5	3.9	408	7	US-11-374-300-20919	Sequence 20919, A
304	86.5	3.9	408	7	US-11-374-300-20922	Sequence 20922, A
305	86.5	3.9	526	7	US-11-374-300-20923	Sequence 20923, A
306	86.5	3.9	526	7	US-11-802-321A-64	Sequence 64, Appl
307	86.5	3.9	526	7	US-11-490-374A-879	Sequence 879, App
308	86.5	3.9	589	7	US-11-490-374A-891	Sequence 891, App
309	86.5	3.9	627	7	US-11-374-300-19170	Sequence 19170, A
310	86.5	3.9	658	1	PCT-US07-18368A-17161	Sequence 17161, A
311	86.5	3.9	670	7	US-11-374-300-13138	Sequence 13138, A
312	86.5	3.9	701	7	US-11-374-300-41008	Sequence 41008, A
313	86.5	3.9	710	7	US-11-374-300-31393	Sequence 31393, A
314	86.5	3.9	742	7	US-11-374-300-24526	Sequence 24526, A
315	86.5	3.9	885	1	US-11-235-701A-232	Sequence 232, App
316	86.5	3.9	885	1	PCT-US07-18368A-27694	Sequence 27694, A
317	86.5	3.9	891	1	PCT-US07-18368A-14244	Sequence 14244, A
318	86.5	3.9	891	7	US-11-374-300-39114	Sequence 39114, A
319	86.5	3.9	969	1	PCT-US07-18368A-1190	Sequence 1190, Ap
320	86.5	3.9	993	1	PCT-US07-18368A-1191	Sequence 1191, Ap
321	86.5	3.9	1029	1	PCT-US07-18368A-19049	Sequence 19049, A
322	86.5	3.9	1136	7	US-11-374-300-7454	Sequence 7454, Ap
323	86.5	3.9	1207	7	US-11-374-300-23353	Sequence 23353, A
324	86.5	3.9	1574	7	US-11-374-300-39357	Sequence 39357, A
325	86.5	3.9	1574	1	PCT-US07-18368A-9029	Sequence 9029, Ap
326	86.5	3.9	1870	1	PCT-US07-18368A-21537	Sequence 21537, A
327	86.5	3.9	1870	7	US-11-374-300-11336	Sequence 11336, A
328	86	3.9	334	1	PCT-US07-18368A-6036	Sequence 6036, Ap
329	86	3.9	381	1	US-11-825-627-300	Sequence 300, App
330	86	3.9	474	1	PCT-US07-18368A-6813	Sequence 6813, Ap
331	86	3.9	527	7	US-11-374-300-41525	Sequence 41525, A
332	86	3.9	586	7	US-11-374-300-40896	Sequence 40896, A
333	86	3.9	621	7	US-11-374-300-47999	Sequence 47999, A
334	86	3.9	628	1	PCT-US07-18368A-6478	Sequence 6478, Ap
335	86	3.9	683	7	US-11-374-300-20861	Sequence 20861, A
336	86	3.9	683	7	US-11-374-300-46072	Sequence 46072, A
337	86	3.9	699	7	US-11-374-300-45826	Sequence 45826, A
338	86	3.9	901	6	US-10-276-032-108	Sequence 108, App
339	86	3.9	1168	7	US-11-374-300-25373	Sequence 25373, A
340	86	3.9	1276	7	US-11-374-300-7949	Sequence 7949, Ap
341	86	3.9	1283	7	US-11-374-300-12934	Sequence 12934, A
342	86	3.9	1340	7	US-11-374-300-20638	Sequence 20638, A
343	86	3.9	1551	7	US-11-374-300-39394	Sequence 39394, A
344	86	3.9	2468	4	PCT-US02-29565-4	Sequence 4, Appli
345	85.5	3.9	446	1	US-11-832-579-19	Sequence 19, Appl
346	85.5	3.9	684	7	US-11-374-300-28433	Sequence 28433, A
347	85.5	3.9	693	7	US-11-374-300-31696	Sequence 31696, A
348	85.5	3.9	748	7	US-11-374-300-9634	Sequence 9634, Ap
349	85.5	3.9	783	7	US-11-374-300-29547	Sequence 29547, A
350	85.5	3.9	800	7	US-11-374-300-12374	Sequence 12374, A
351	85.5	3.9	800	7	US-11-374-300-35839	Sequence 35839, A
352	85.5	3.9	868	7	US-11-374-300-47496	Sequence 47496, A
353	85.5	3.9	870	7	US-11-374-300-37945	Sequence 37945, A
354	85.5	3.9	891	1	PCT-US07-18368A-23239	Sequence 23239, A
355	85.5	3.9	891	7	US-11-374-300-20903	Sequence 20903, A
356	85.5	3.9	1359	7	US-11-374-300-46236	Sequence 46236, A
357	85.5	3.9	1651	7	US-11-374-300-47768	Sequence 47768, A
358	85.5	3.9	1822	7	US-11-490-374A-427	Sequence 427, App
359	85.5	3.9	1822	7	US-11-490-374A-429	Sequence 429, App
360	85.5	3.9	1822	7	US-11-490-374A-430	Sequence 430, App
361	85.5	3.9	1822	7	US-11-490-374A-434	Sequence 434, App
362	85	3.8	328	7	US-11-884-546-69	Sequence 69, Appl
363	85	3.8	407	1	US-11-883-996-18	Sequence 18, Appl
364	85	3.8	453	7	US-11-374-300-28361	Sequence 28361, A
365	85	3.8	706	7	US-11-374-300-43953	Sequence 43953, A
366	85	3.8	706	1	PCT-US07-18368A-6965	Sequence 6965, Ap
367	85	3.8	10203	7	US-11-665-940-32	Sequence 32, Appl
368	84.5	3.8	217	7	US-11-374-300-9364	Sequence 9364, Ap
369	84.5	3.8	385	7	US-11-374-300-15268	Sequence 15268, A
370	84.5	3.8	387	7	US-11-374-300-48300	Sequence 48300, A
371	84.5	3.8	561	7	US-11-374-300-45279	Sequence 45279, A
372	84.5	3.8	634	7	US-11-374-300-43234	Sequence 43234, A
373	84.5	3.8	640	7	US-11-884-546-69	Sequence 69, Appl
374	84.5	3.8	668	7	US-11-374-300-40209	Sequence 40209, A
375	84.5	3.8	672	7	US-11-374-300-49216	Sequence 49216, A
376	84.5	3.8	676	7	US-11-374-300-40138	Sequence 40138, A
377	84.5	3.8	699	1	US-11-235-701A-231	Sequence 231, App
378	84.5	3.8	700	1	US-11-235-701A-228	Sequence 228, App
379	84.5	3.8	742	1	US-11-235-701A-229	Sequence 229, App
380	84.5	3.8	743	1	US-11-235-701A-226	Sequence 226, App
381	84.5	3.8	743	1	US-11-235-701A-240	Sequence 240, App
382	84.5	3.8	775	1	PCT-US07-18368A-7629	Sequence 7629, Ap
383	84.5	3.8	775	7	US-11-374-300-7559	Sequence 7559, Ap
384	84.5	3.8	979	1	PCT-US07-18368A-4606	Sequence 4606, Ap
385	84.5	3.8	979	7	US-11-374-300-29016	Sequence 29016, A
386	84	3.8	332	1	PCT-US07-18368A-12412	Sequence 12412, A
387	84	3.8	522	7	US-11-374-300-24644	Sequence 24644, A
388	84	3.8	561	7	US-11-374-300-36202	Sequence 36202, A
389	84	3.8	635	1	PCT-US07-18368A-28291	Sequence 28291, A
390	84	3.8	664	7	US-11-374-300-4499	Sequence 4499, Ap

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391	3.8	669	US-11-235-701A-234	7	84	Sequence 234, App
392	3.8	718	US-11-374-300-6871	7	84	Sequence 6871, Ap
393	3.8	733	US-11-490-374A-239	7	84	Sequence 239, App
394	3.8	733	US-11-490-374A-240	7	84	Sequence 240, App
395	3.8	733	US-11-490-374A-241	7	84	Sequence 241, App
396	3.8	927	PCT-US07-18368A-9980	1	84	Sequence 9980, Ap
397	3.8	1037	PCT-US07-18368A-26323	1	84	Sequence 26323, A
398	3.8	1037	PCT-US07-18368A-23705	1	84	Sequence 23705, A
399	3.8	1071	PCT-US07-18368A-25049	1	84	Sequence 25049, A
400	3.8	1071	US-11-374-300-22579	7	84	Sequence 22579, A
401	3.8	2446	US-11-490-374A-283	7	84	Sequence 283, App
402	3.8	2477	US-11-490-374A-273	7	84	Sequence 273, App
403	3.8	2477	US-11-490-374A-280	7	84	Sequence 280, App
404	3.8	373	US-11-560-103-5	6	83.5	Sequence 5, Appli
405	3.8	390	US-11-374-300-36344	7	83.5	Sequence 36344, A
406	3.8	550	US-11-374-300-44590	7	83.5	Sequence 44590, A
407	3.8	553	US-11-374-300-42482	7	83.5	Sequence 42482, A
408	3.8	561	US-11-374-300-30042	7	83.5	Sequence 30042, A
409	3.8	561	US-11-374-300-36778	7	83.5	Sequence 36778, A
410	3.8	562	US-11-374-300-16619	7	83.5	Sequence 16619, A
411	3.8	581	US-11-825-627-98	7	83.5	Sequence 98, Appl
412	3.8	596	US-11-374-300-46091	7	83.5	Sequence 46091, A
413	3.8	596	US-11-374-300-49855	7	83.5	Sequence 49855, A
414	3.8	668	US-11-374-300-44853	7	83.5	Sequence 44853, A
415	3.8	695	US-11-374-300-42254	7	83.5	Sequence 42254, A
416	3.8	700	US-11-374-300-43062	7	83.5	Sequence 43062, A
417	3.8	822	US-11-374-300-32928	7	83.5	Sequence 32928, A
418	3.8	835	US-11-374-300-5250	7	83.5	Sequence 5250, Ap
419	3.8	1238	US-11-374-300-5591	7	83.5	Sequence 5591, Ap
420	3.8	1238	US-11-374-300-8996	7	83.5	Sequence 8996, Ap
421	3.8	1238	US-11-374-300-24842	7	83.5	Sequence 24842, A
422	3.8	1238	US-11-374-300-48166	7	83.5	Sequence 48166, A
423	3.8	1847	US-11-374-300-15620	7	83.5	Sequence 15620, A
424	3.8	1919	US-11-374-300-19214	7	83.5	Sequence 19214, A
425	3.8	2421	US-11-490-374A-270	7	83.5	Sequence 270, App
426	3.8	2421	US-11-490-374A-272	7	83.5	Sequence 272, App
427	3.8	346	US-60-970-876-56	8	83	Sequence 56, Appl
428	3.8	395	PCT-US07-18368A-1598	1	83	Sequence 1598, Ap
429	3.8	403	US-11-374-300-12161	7	83	Sequence 12161, A
430	3.8	426	PCT-US07-18368A-2843	1	83	Sequence 2843, Ap
431	3.8	446	US-11-374-300-32626	7	83	Sequence 32626, A
432	3.8	507	US-11-374-300-32602	7	83	Sequence 32602, A
433	3.8	552	PCT-US07-18368A-24429	1	83	Sequence 24429, A
434	3.8	559	US-11-374-300-13216	7	83	Sequence 13216, A
435	3.8	559	US-11-374-300-49806	7	83	Sequence 49806, A
436	3.8	608	US-11-374-300-7736	7	83	Sequence 7736, Ap
437	3.8	608	US-11-374-300-32362	7	83	Sequence 32362, A
438	3.8	636	US-11-374-300-2813	7	83	Sequence 2813, Ap
439	3.8	873	US-11-374-300-37366	7	83	Sequence 37366, A
440	3.8	886	US-11-374-300-49084	7	83	Sequence 49084, A
441	3.8	1068	PCT-US07-18368A-13085	1	83	Sequence 13085, A
442	3.8	3896	US-11-374-300-12173	1	82.5	Sequence 12173, A
443	3.7	270	US-11-883-996-75	7	82.5	Sequence 75, Appl
444	3.7	350	US-11-490-374A-244	7	82.5	Sequence 244, App
445	3.7	492	PCT-US07-18368A-10316	1	82.5	Sequence 10316, A
446	3.7	545	PCT-US07-18368A-9874	1	82.5	Sequence 9874, Ap
447	3.7	559	PCT-US07-18368A-12980	1	82.5	Sequence 12980, A
448	3.7	811	US-11-374-300-16711	7	82.5	Sequence 16711, A
449	3.7	873	PCT-US07-18368A-16571	1	82.5	Sequence 16571, A
450	3.7	925	US-11-374-300-12075	7	82.5	Sequence 12075, A
451	3.7	987	PCT-US07-18368A-25051	1	82.5	Sequence 25051, A
452	3.7	1224	US-11-374-300-19786	7	82.5	Sequence 19786, A
453	3.7	1364	US-11-374-300-4660	7	82.5	Sequence 4660, Ap
454	3.7	7257	US-11-374-300-47395	7	82.5	Sequence 47395, A
455	3.7	414	US-11-374-300-34856	7	82	Sequence 34856, A
456	3.7	418	US-11-490-374A-244	7	82	Sequence 244, App
457	3.7	569	PCT-US07-18368A-16024	1	82	Sequence 16024, A
458	3.7	647	PCT-US07-18368A-23852	1	82	Sequence 23852, A
459	3.7	693	US-11-374-300-40451	7	82	Sequence 40451, A
460	3.7	779	US-11-374-300-9538	7	82	Sequence 9538, Ap
461	3.7	817	PCT-US07-18368A-8832	1	82	Sequence 8832, Ap
462	3.7	817	US-11-374-300-29227	7	82	Sequence 29227, A
463	3.7	822	US-11-374-300-22611	7	82	Sequence 22611, A

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464	82	3.7	1633	PCT-US07-18368A-18647	1	Sequence 18647, A
465	82	3.7	1764	PCT-US07-18368A-26691	1	Sequence 26691, A
466	82	3.7	1764	US-11-374-300-49497	7	Sequence 49497, A
467	82	3.7	1902	US-11-825-627-321	7	Sequence 321, App
468	82	3.7	1914	US-11-374-300-45371	7	Sequence 45371, A
469	81.5	3.7	394	US-11-374-300-10575	7	Sequence 10575, A
470	81.5	3.7	441	US-11-374-300-26432	7	Sequence 26432, A
471	81.5	3.7	443	US-11-374-300-11276	7	Sequence 11276, A
472	81.5	3.7	468	PCT-US07-18368A-26733	1	Sequence 26733, A
473	81.5	3.7	492	PCT-US07-18368A-10350	1	Sequence 10350, A
474	81.5	3.7	516	US-11-374-300-46425	7	Sequence 46425, A
475	81.5	3.7	532	PCT-US07-18368A-8293	1	Sequence 8293, Ap
476	81.5	3.7	692	US-11-908-114-35	7	Sequence 35, Appl
477	81.5	3.7	774	US-11-374-300-16222	7	Sequence 16222, A
478	81.5	3.7	798	US-11-374-300-29444	7	Sequence 29444, A
479	81.5	3.7	805	US-11-374-300-21352	7	Sequence 21352, A
480	81.5	3.7	808	US-11-374-300-20391	7	Sequence 20391, A
481	81.5	3.7	871	PCT-US07-18368A-20829	1	Sequence 20829, Ap
482	81.5	3.7	928	PCT-US07-18368A-6779	1	Sequence 6779, Ap
483	81.5	3.7	946	PCT-US07-18368A-18326	1	Sequence 18326, A
484	81.5	3.7	1120	US-11-374-300-16557	7	Sequence 16537, A
485	81.5	3.7	1302	US-11-374-300-24340	7	Sequence 24340, A
486	81.5	3.7	1518	PCT-US07-18368A-30282	1	Sequence 30282, A
487	81.5	3.7	1518	US-11-374-300-27391	7	Sequence 27391, A
488	81.5	3.7	2544	US-11-374-300-16996	7	Sequence 16996, A
489	81.5	3.7	7257	US-11-374-300-44001	7	Sequence 44001, A
490	81.5	3.7	196	US-11-374-300-42661	7	Sequence 42661, A
491	81	3.7	235	US-11-665-940-29	7	Sequence 29, Appl
492	81	3.7	275	US-11-781-818-62	7	Sequence 62, Appl
493	81	3.7	399	US-11-374-300-6866	7	Sequence 6866, Ap
494	81	3.7	399	US-11-374-300-8263	7	Sequence 8263, Ap
495	81	3.7	399	US-11-374-300-16233	7	Sequence 16233, A
496	81	3.7	410	US-11-490-374A-389	7	Sequence 389, App
497	81	3.7	410	US-11-490-374A-392	7	Sequence 392, App
498	81	3.7	478	PCT-US07-18368A-9609	1	Sequence 9609, Ap
499	81	3.7	481	US-11-374-300-45877	7	Sequence 45877, A
500	81	3.7	492	PCT-US07-18368A-10318	1	Sequence 10318, A
501	81	3.7	646	PCT-US07-18368A-8988	1	Sequence 8988, Ap
502	81	3.7	682	US-11-374-300-24827	7	Sequence 24827, A
503	81	3.7	698	US-11-374-300-19725	7	Sequence 19725, A
504	81	3.7	698	US-11-374-300-42041	7	Sequence 42041, A
505	81	3.7	760	PCT-US07-18368A-23849	1	Sequence 23849, A
506	81	3.7	790	PCT-US07-18368A-12920	1	Sequence 12920, A
507	81	3.7	799	PCT-US07-18368A-3608	1	Sequence 3608, Ap
508	81	3.7	800	PCT-US07-18368A-17020	1	Sequence 17020, A
509	81	3.7	917	PCT-US07-18368A-13576	1	Sequence 13576, A
510	81	3.7	917	US-11-374-300-22139	7	Sequence 22139, A
511	81	3.7	933	PCT-US07-18368A-28900	1	Sequence 28900, A
512	81	3.7	1033	US-11-374-300-44149	7	Sequence 4149, A
513	81	3.7	1103	PCT-US07-18368A-8791	1	Sequence 8791, Ap
514	81	3.7	1103	US-11-374-300-8564	7	Sequence 8564, Ap
515	81	3.7	1142	PCT-US07-18368A-22566	1	Sequence 22566, A
516	81	3.7	1142	US-11-374-300-17058	7	Sequence 17058, A
517	81	3.7	1147	PCT-US07-18368A-28101	1	Sequence 28101, A
518	81	3.7	1147	US-11-374-300-36434	7	Sequence 36434, A
519	81	3.7	1176	PCT-US07-18368A-16060	1	Sequence 16060, A
520	81	3.7	1236	US-11-374-300-11064	7	Sequence 11064, A
521	81	3.7	1733	PCT-US07-18368A-28256	1	Sequence 28256, A
522	80.5	3.6	421	US-11-374-300-20317	7	Sequence 20317, A
523	80.5	3.6	426	US-11-374-300-41225	7	Sequence 41225, A
524	80.5	3.6	495	PCT-US07-18368A-27191	1	Sequence 27191, A
525	80.5	3.6	518	PCT-US07-13803-552	7	Sequence 552, App
526	80.5	3.6	518	PCT-US07-13803-792	7	Sequence 792, APP
527	80.5	3.6	558	US-11-374-300-49909	7	Sequence 49909, A
528	80.5	3.6	559	PCT-US07-13803-736	7	Sequence 736, APP
529	80.5	3.6	559	PCT-US07-13803-793	7	Sequence 793, App
530	80.5	3.6	616	PCT-US07-18368A-17712	1	Sequence 17712, A
531	80.5	3.6	619	US-11-374-300-11044	7	Sequence 11044, A
532	80.5	3.6	632	PCT-US07-18368A-3775	1	Sequence 3775, Ap
533	80.5	3.6	675	US-11-374-300-18051	7	Sequence 18051, A
534	80.5	3.6	676	US-11-374-300-9697	7	Sequence 9697, Ap
535	80.5	3.6	713	US-11-374-300-15016	7	Sequence 15016, A
536	80.5	3.6	743	US-11-374-300-21663	7	Sequence 21663, A

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537	80.5	3.6	868	US-11-374-300-18873	Sequence 18873, A
538	80.5	3.6	924	US-11-374-300-22418	Sequence 22418, A
539	80.5	3.6	953	PCT-US07-18368A-19633	Sequence 19633, Ap
540	80.5	3.6	1238	US-11-374-300-8817	Sequence 8817, Ap
541	80.5	3.6	1238	US-11-374-300-14150	Sequence 14150, A
542	80.5	3.6	1273	US-11-374-300-35873	Sequence 35873, A
543	80.5	3.6	2072	US-11-374-300-35793	Sequence 35793, A
544	80	3.6	216	PCT-US07-18368A-12054	Sequence 12054, A
545	80	3.6	216	US-11-374-300-11415	Sequence 11415, A
546	80	3.6	335	US-11-374-13803-553	Sequence 553, App
547	80	3.6	379	PCT-US07-18368A-2680	Sequence 2680, Ap
548	80	3.6	387	US-11-490-374A-242	Sequence 242, App
549	80	3.6	414	US-11-374-300-23931	Sequence 23931, A
550	80	3.6	423	US-11-374-300-5767	Sequence 5767, Ap
551	80	3.6	441	US-11-883-197-1	Sequence 1, Appli
552	80	3.6	466	PCT-US07-18368A-27937	Sequence 27937, A
553	80	3.6	514	US-11-374-300-19525	Sequence 19525, A
554	80	3.6	572	US-11-374-300-22936	Sequence 22936, A
555	80	3.6	601	US-11-374-300-17092	Sequence 17092, A
556	80	3.6	646	US-11-374-300-41167	Sequence 41167, A
557	80	3.6	655	US-11-374-300-23867	Sequence 23867, A
558	80	3.6	737	US-11-374-300-41134	Sequence 41134, A
559	80	3.6	766	PCT-US07-18368A-3910	Sequence 3910, Ap
560	80	3.6	956	US-11-374-300-37360	Sequence 37360, A
561	80	3.6	1042	US-11-354-210-109	Sequence 109, App
562	80	3.6	1341	PCT-US07-18368A-5717	Sequence 5717, Ap
563	80	3.6	1341	US-11-374-300-40098	Sequence 40098, A
564	80	3.6	1875	US-11-490-374A-428	Sequence 428, App
565	80	3.6	1875	US-11-490-374A-433	Sequence 433, App
566	80	3.6	2679	US-11-374-300-37742	Sequence 37742, A
567	79.5	3.6	225	US-11-374-300-43354	Sequence 43354, A
568	79.5	3.6	355	US-11-374-300-28180	Sequence 28180, A
569	79.5	3.6	360	US-11-831-404-121	Sequence 121, App
570	79.5	3.6	360	US-11-831-404-135	Sequence 135, App
571	79.5	3.6	410	US-11-490-374A-391	Sequence 391, App
572	79.5	3.6	410	US-11-490-374A-393	Sequence 393, App
573	79.5	3.6	428	PCT-US07-18368A-21288	Sequence 21288, A
574	79.5	3.6	438	US-11-880-377-2458	Sequence 2458, Ap
575	79.5	3.6	486	US-11-816-233-139	Sequence 139, App
576	79.5	3.6	500	US-11-825-627-7	Sequence 7, Appli
577	79.5	3.6	526	US-11-374-300-32386	Sequence 32386, A
578	79.5	3.6	560	US-11-374-300-18946	Sequence 18946, A
579	79.5	3.6	573	US-11-374-300-47891	Sequence 47891, A
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586	79.5	3.6	717	US-11-374-300-18034	Sequence 18034, A
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588	79.5	3.6	894	US-11-374-300-31780	Sequence 31780, A
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590	79.5	3.6	922	US-11-374-300-22416	Sequence 22416, A
591	79.5	3.6	955	PCT-US07-18368A-15271	Sequence 15271, A
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593	79.5	3.6	1102	US-11-374-300-45022	Sequence 45022, A
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595	79.5	3.6	1104	US-11-374-300-13775	Sequence 13775, A
596	79.5	3.6	1136	US-11-374-300-25566	Sequence 25566, A
597	79	3.6	210	US-11-374-300-9089	Sequence 9089, Ap
598	79	3.6	295	PCT-US07-18368A-29756	Sequence 29756, A
599	79	3.6	347	US-11-374-300-41662	Sequence 41662, A
600	79	3.6	392	US-11-374-300-16051	Sequence 16051, A
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602	79	3.6	441	US-11-834-897-48	Sequence 48, Appl
603	79	3.6	486	US-11-816-233-138	Sequence 138, App
604	79	3.6	502	US-11-374-300-33814	Sequence 33814, A
605	79	3.6	514	PCT-US07-18368A-8688	Sequence 8688, Ap
606	79	3.6	514	US-11-374-300-34667	Sequence 34667, A
607	79	3.6	529	PCT-US07-18368A-11607	Sequence 11607, A
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609	79	3.6	571	US-11-374-300-33896	Sequence 33896, A

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613	79	3.6	710	PCT-US07-18368A-11546	1	Sequence 11546, A
614	79	3.6	734	PCT-US07-18368A-475	1	Sequence 475, App
615	79	3.6	867	PCT-US07-18368A-4612	1	Sequence 4612, Ap
616	79	3.6	867	US-11-374-300-21641	7	Sequence 21641, A
617	79	3.6	914	US-11-374-300-13001	7	Sequence 13001, A
618	79	3.6	979	US-11-490-374A-35	7	Sequence 35, Appl
619	79	3.6	988	US-11-490-374A-29	7	Sequence 29, Appl
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621	79	3.6	1230	PCT-US07-18368A-17130	1	Sequence 17130, A
622	79	3.6	1230	US-11-374-300-9718	7	Sequence 9718, Ap
623	79	3.6	1230	US-11-374-300-15845	7	Sequence 15845, A
624	79	3.6	1286	US-11-374-300-26644	7	Sequence 26644, A
625	79	3.6	1703	PCT-US07-18368A-13497	1	Sequence 13497, A
626	79	3.6	2101	US-11-490-374A-27	7	Sequence 27, Appl
627	79	3.6	2101	US-11-490-374A-32	7	Sequence 32, Appl
628	79	3.6	2110	US-11-490-374A-34	7	Sequence 34, Appl
629	79	3.6	2115	US-11-490-374A-26	7	Sequence 26, Appl
630	79	3.6	2115	US-11-490-374A-36	7	Sequence 36, Appl
631	79	3.6	2124	US-11-490-374A-31	7	Sequence 31, Appl
632	78.5	3.6	360	US-11-831-404-123	7	Sequence 123, App
633	78.5	3.6	365	US-11-186-807A-28	7	Sequence 28, Appl
634	78.5	3.6	434	US-11-816-601-215	7	Sequence 215, App
635	78.5	3.6	434	PCT-US07-18368A-36502	1	Sequence 36502, A
636	78.5	3.6	498	US-11-801-963A-2949	7	Sequence 2949, Ap
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638	78.5	3.6	529	US-11-374-300-4389	7	Sequence 4389, Ap
639	78.5	3.6	529	US-11-374-300-14574	7	Sequence 14574, A
640	78.5	3.6	536	US-11-235-701A-239	7	Sequence 239, App
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645	78.5	3.6	644	US-11-374-300-24351	7	Sequence 24351, A
646	78.5	3.6	658	US-11-374-300-23831	7	Sequence 23831, A
647	78.5	3.6	658	US-11-374-300-32949	7	Sequence 32949, A
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649	78.5	3.6	757	US-11-374-300-27733	7	Sequence 27733, A
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660	78.5	3.6	1162	US-11-374-300-29858	7	Sequence 29858, A
661	78.5	3.6	1296	US-11-374-300-9526	7	Sequence 9526, Ap
662	78.5	3.6	1296	US-11-374-300-36888	7	Sequence 36888, A
663	78.5	3.6	1421	US-11-374-300-47377	7	Sequence 47377, A
664	78.5	3.6	1464	US-11-816-601-751	7	Sequence 751, App
665	78	3.5	333	US-11-374-300-8590	7	Sequence 8590, Ap
666	78	3.5	335	US-11-374-300-11672	7	Sequence 11672, A
667	78	3.5	342	US-60-970-876-44	8	Sequence 44, Appl
668	78	3.5	348	PCT-US07-18368A-8198	1	Sequence 8198, Ap
669	78	3.5	426	US-11-374-300-37761	7	Sequence 37761, A
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672	78	3.5	492	PCT-US07-18368A-10320	1	Sequence 10320, A
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676	78	3.5	543	US-11-816-233-222	7	Sequence 222, App
677	78	3.5	555	PCT-US07-18368A-20177	1	Sequence 20177, A
678	78	3.5	573	US-11-374-300-31918	7	Sequence 31918, A
679	78	3.5	586	US-11-834-332-6	7	Sequence 6, Appli
680	78	3.5	609	PCT-US07-18368A-12570	1	Sequence 12570, A
681	78	3.5	644	US-11-374-300-1161	7	Sequence 1161, Ap
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683	3.5	78	683	US-11-374-300-39279	7	Sequence 39279, A
684	3.5	78	692	US-11-235-701A-227	7	Sequence 227, App
685	3.5	78	724	US-11-374-300-22608	7	Sequence 22608, A
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687	3.5	78	765	US-11-374-300-39915	7	Sequence 39915, A
688	3.5	78	816	US-11-374-300-1730	7	Sequence 1730, Ap
689	3.5	78	907	US-11-374-300-15095	7	Sequence 15095, A
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696	3.5	78	929	US-11-374-300-7438	7	Sequence 7438, Ap
697	3.5	78	1097	PCT-US07-18368A-9490	1	Sequence 9490, Ap
698	3.5	78	1462	PCT-US07-18368A-14854	1	Sequence 14854, A
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703	3.5	77.5	285	US-11-374-300-35101	7	Sequence 35101, A
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706	3.5	77.5	421	PCT-US07-18368A-26487	1	Sequence 26487, A
707	3.5	77.5	434	US-11-374-300-30929	7	Sequence 30929, A
708	3.5	77.5	479	US-11-374-300-25408	7	Sequence 25408, A
709	3.5	77.5	486	US-11-816-233-150	7	Sequence 150, App
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711	3.5	77.5	519	US-11-374-300-21247	7	Sequence 21247, A
712	3.5	77.5	561	US-11-374-300-29416	7	Sequence 29416, A
713	3.5	77.5	567	US-11-374-300-8299	7	Sequence 8299, Ap
714	3.5	77.5	570	US-11-374-300-17179	7	Sequence 17179, A
715	3.5	77.5	632	PCT-US07-18368A-21806	1	Sequence 21806, A
716	3.5	77.5	669	US-10-563-758-4	6	Sequence 4, Appli
717	3.5	77.5	688	US-11-374-300-5826	7	Sequence 5826, Ap
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721	3.5	77.5	848	US-11-374-300-18143	7	Sequence 18143, A
722	3.5	77.5	901	US-11-374-300-18323	7	Sequence 18323, A
723	3.5	77.5	1044	US-11-732-856-3	7	Sequence 3, Appli
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727	3.5	77	287	US-11-374-300-11867	7	Sequence 11867, Ap
728	3.5	77	319	US-11-374-300-29106	7	Sequence 29106, A
729	3.5	77	327	US-11-374-300-31188	7	Sequence 31188, A
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731	3.5	77	358	PCT-US07-18368A-22834	1	Sequence 22834, A
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738	3.5	77	719	US-11-374-300-48694	7	Sequence 48694, A
739	3.5	77	793	US-11-374-300-27812	7	Sequence 27812, A
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742	3.5	77	957	PCT-US07-18368A-17002	1	Sequence 17002, A
743	3.5	77	1107	US-11-374-300-14607	7	Sequence 14607, A
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746	3.5	77	1361	US-11-816-601-244	7	Sequence 244, Appl
747	3.5	77	1885	US-10-741-191B-22	6	Sequence 22, Appl
748	3.5	77	1955	PCT-US07-18368A-11207	1	Sequence 11207, A
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751	3.5	76.5	421	US-11-801-963A-2907	7	Sequence 2907, Ap
752	3.5	76.5	442	US-11-802-321A-14	7	Sequence 14, Appl
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754	3.5	76.5	519	US-11-374-300-24278	7	Sequence 24278, A
755	3.5	76.5	561	US-11-374-300-31849	7	Sequence 31849, A
756	3.5	76.5	597	US-11-374-300-21695	7	Sequence 21695, A
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763	3.5	76.5	729	US-11-374-300-10667	7	Sequence 10667, A
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766	3.5	76.5	909	PCT-US07-18368A-22487	1	Sequence 22487, A
767	3.5	76.5	952	US-11-374-300-2227	7	Sequence 2227, A
768	3.5	76.5	964	PCT-US07-18368A-27572	1	Sequence 27572, A
769	3.5	76.5	984	PCT-US07-13803-628	1	Sequence 628, App
770	3.5	76.5	1017	US-11-374-300-29504	7	Sequence 29504, A
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773	3.5	76.5	1192	US-11-490-374A-97	7	Sequence 97, Appli
774	3.5	76.5	1208	PCT-US07-18368A-16370	1	Sequence 16370, A
775	3.5	76.5	1208	PCT-US07-18368A-15110	1	Sequence 15110, A
776	3.5	76.5	1832	PCT-US07-18368A-17029	1	Sequence 17029, A
777	3.5	76.5	1832	US-11-374-300-15761	7	Sequence 15761, A
778	3.5	76.5	2761	PCT-US07-18368A-21820	1	Sequence 21820, A
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788	3.4	76	497	US-11-431-794-34	7	Sequence 34, Appl
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791	3.4	76	560	US-11-374-300-1402	7	Sequence 1402, Ap
792	3.4	76	578	PCT-US07-76897-3	7	Sequence 3, Appl
793	3.4	76	578	PCT-US07-76899-5	7	Sequence 5, Appli
794	3.4	76	578	PCT-US07-76892-5	7	Sequence 5, Appli
795	3.4	76	588	PCT-US07-18368A-4517	1	Sequence 4517, Ap
796	3.4	76	588	US-11-374-300-28007	7	Sequence 28007, A
797	3.4	76	636	PCT-US07-76899-34	7	Sequence 34, Appl
798	3.4	76	636	PCT-US07-76892-34	7	Sequence 34, Appl
799	3.4	76	637	PCT-US07-18368A-26358	1	Sequence 26358, A
800	3.4	76	647	US-11-374-300-7691	7	Sequence 7691, Ap
801	3.4	76	650	US-11-374-300-5291	7	Sequence 5291, Ap
802	3.4	76	680	US-11-374-300-6949	7	Sequence 6949, Ap
803	3.4	76	683	US-11-374-300-49690	7	Sequence 49690, A
804	3.4	76	724	US-11-374-300-44362	7	Sequence 44362, A
805	3.4	76	738	US-11-374-300-48784	7	Sequence 48784, A
806	3.4	76	789	US-11-490-374A-238	7	Sequence 238, Appl
807	3.4	76	814	US-11-490-374A-39	7	Sequence 39, Appl
808	3.4	76	814	US-11-490-374A-41	7	Sequence 41, Appl
809	3.4	76	833	US-11-374-300-5150	7	Sequence 5150, Ap
810	3.4	76	858	US-11-060-659A-48	7	Sequence 48, Appl
811	3.4	76	858	US-11-490-374A-40	7	Sequence 40, Appl
812	3.4	76	858	US-11-490-374A-43	7	Sequence 43, Appl
813	3.4	76	858	US-11-490-374A-44	7	Sequence 44, Appl
814	3.4	76	860	US-11-490-374A-45	7	Sequence 45, Appl
815	3.4	76	894	US-11-374-300-1406	7	Sequence 1406, Ap
816	3.4	76	894	US-11-374-300-13134	7	Sequence 13134, A
817	3.4	76	903	PCT-US07-13803-715	1	Sequence 715, App
818	3.4	76	903	US-10-490-605B-2	6	Sequence 2, Appli
819	3.4	76	916	US-11-374-300-35542	7	Sequence 35542, A
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822	3.4	76	1212	PCT-US07-18368A-1904	1	Sequence 1904, Ap
823	3.4	76	1212	US-11-374-300-2537	7	Sequence 2537, Ap
824	3.4	76	1646	US-60-971-637-23	8	Sequence 23, Appl
825	3.4	76	1647	US-60-971-637-24	8	Sequence 24, Appl
826	3.4	76	1649	US-60-971-637-40	8	Sequence 40, Appl
827	3.4	76	1649	US-60-971-637-41	8	Sequence 41, Appl
828	3.4	76	1649	US-60-971-637-42	8	Sequence 42, Appl

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834	3.4	76	2059	7	US-11-781-871-16	Sequence 16, Appl
835	3.4	76	2059	7	US-11-781-874-16	Sequence 16, Appl
836	3.4	76	2059	7	US-11-781-875-16	Sequence 16, Appl
837	3.4	76	2059	7	US-11-781-877-16	Sequence 16, Appl
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849	3.4	75.5	350	7	US-11-374-300-20630	Sequence 20630, A
850	3.4	75.5	363	7	US-11-374-300-36846	Sequence 36846, A
851	3.4	75.5	364	7	US-11-374-300-24013	Sequence 24013, A
852	3.4	75.5	382	7	US-11-374-300-28100	Sequence 28100, A
853	3.4	75.5	395	7	US-11-374-300-26317	Sequence 26317, A
854	3.4	75.5	421	1	PCT-US07-18368A-12309	Sequence 12309, A
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856	3.4	75.5	436	7	US-11-374-300-33173	Sequence 33173, A
857	3.4	75.5	467	7	US-11-374-300-21607	Sequence 21607, A
858	3.4	75.5	506	7	US-11-374-300-32155	Sequence 32155, A
859	3.4	75.5	514	7	US-11-374-300-34557	Sequence 34557, A
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899	3.4	75.5	2020	7	US-11-781-870-10	Sequence 10, Appl
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904	75.5	3.4	2020	7	US-11-781-882-10	Sequence 10, Appl
905	75	3.4	275	7	US-11-374-300-23029	Sequence 23029, A
906	75	3.4	340	7	US-11-374-300-46827	Sequence 46827, A
907	75	3.4	348	7	US-11-846-663-11	Sequence 11, Appl
908	75	3.4	359	7	US-11-374-300-24478	Sequence 24478, A
909	75	3.4	405	7	US-11-781-665-6164	Sequence 6164, Ap
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912	75	3.4	462	7	US-11-374-300-25651	Sequence 25651, A
913	75	3.4	484	1	PCT-US07-18368A-24237	Sequence 24237, A
914	75	3.4	486	7	US-11-816-233-223	Sequence 223, App
915	75	3.4	520	7	US-11-374-300-17986	Sequence 17986, A
916	75	3.4	533	7	US-11-374-300-26992	Sequence 26992, A
917	75	3.4	534	7	US-11-374-300-11707	Sequence 11707, A
918	75	3.4	559	7	US-11-374-300-30098	Sequence 30098, A
919	75	3.4	568	7	US-11-374-300-25036	Sequence 25036, A
920	75	3.4	574	7	US-11-374-300-4405	Sequence 4405, Ap
921	75	3.4	576	7	US-11-374-300-38328	Sequence 38328, A
922	75	3.4	676	1	PCT-US07-18368A-16895	Sequence 16895, A
923	75	3.4	714	7	US-11-374-300-5977	Sequence 5977, Ap
924	75	3.4	714	7	US-11-374-300-29183	Sequence 29183, A
925	75	3.4	735	1	PCT-US07-18368A-27642	Sequence 27642, A
926	75	3.4	759	1	PCT-US07-18368A-28017	Sequence 28017, A
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928	75	3.4	764	7	US-11-374-300-39241	Sequence 39241, A
929	75	3.4	793	7	US-11-374-300-20160	Sequence 20160, A
930	75	3.4	850	7	US-11-795-915-325	Sequence 325, App
931	75	3.4	902	1	PCT-US07-18368A-17513	Sequence 17513, A
932	75	3.4	902	7	US-11-374-300-16167	Sequence 16167, A
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934	75	3.4	1170	7	US-11-374-300-29173	Sequence 29173, A
935	75	3.4	1235	7	US-11-836-563-27	Sequence 27, Appl
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937	74.5	3.4	1437	1	US-11-816-601-187	Sequence 187, App
938	74.5	3.4	1437	1	US-11-816-601-322	Sequence 322, App
939	74.5	3.4	1437	1	US-11-816-601-763	Sequence 763, App
940	74.5	3.4	1437	1	US-11-816-601-837	Sequence 837, App
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968	74.5	3.4	609	7	US-11-374-300-6555	Sequence 6555, Ap
969	74.5	3.4	629	7	US-11-374-300-5635	Sequence 5635, Ap
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979	74	3.3	252	US-11-374-300-33001	7	Sequence 33001, A
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992	74	3.3	459	US-11-374-300-32042	7	Sequence 32042, A
993	74	3.3	460	PCT-US07-18368A-30242	1	Sequence 30242, A
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998	74	3.3	516	US-11-374-300-21900	7	Sequence 21900, A
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1046	73.5	3.3	417	PCT-US07-18368A-8180	1	Sequence 8180, Ap
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1049	73.5	3.3	486	US-11-816-233-151	7	Sequence 151, App
1050	73.5	3.3	494	US-11-374-300-37512	7	Sequence 37512, A
1051	73.5	3.3	526	PCT-US07-13803-603	7	Sequence 603, App
1052	73.5	3.3	527	PCT-US07-18368A-14672	1	Sequence 14672, A
1053	73.5	3.3	534	US-11-374-300-11251	7	Sequence 11251, A
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1055	73.5	3.3	561	US-11-374-300-6547	7	Sequence 6547, Ap
1056	73.5	3.3	582	US-11-374-300-27722	7	Sequence 27722, A
1057	73.5	3.3	597	US-11-374-300-28071	7	Sequence 28071, A
1058	73.5	3.3	600	US-11-374-300-25453	7	Sequence 25453, A
1059	73.5	3.3	650	US-11-374-300-10372	7	Sequence 10372, A
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1062	73.5	3.3	688	US-11-374-300-13695	7	Sequence 13695, A
1063	73.5	3.3	692	US-11-374-300-45691	7	Sequence 45691, A
1064	73.5	3.3	715	US-11-374-300-49809	7	Sequence 49809, A
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1067	73.5	3.3	806	US-11-834-897-47	7	Sequence 47, Appl
1068	73.5	3.3	817	US-11-374-300-9476	7	Sequence 9476, Ap
1069	73.5	3.3	834	US-11-374-300-27932	7	Sequence 27932, A
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1071	73	3.3	922	PCT-US07-18368A-10926	1	Sequence 10926, A
1072	73	3.3	947	PCT-US07-18368A-17723	1	Sequence 17723, A
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1074	73	3.3	957	US-60-911-843A-14	8	Sequence 14, Appl
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1079	73	3.3	1086	US-11-374-300-30603	7	Sequence 30603, A
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1081	73	3.3	1123	US-11-374-300-24244	7	Sequence 24244, A
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1086	73	3.3	3979	US-11-374-300-29467	7	Sequence 29467, A
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1091	73	3.3	410	PCT-US07-18368A-21508	1	Sequence 21508, A
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1104	73	3.3	592	US-11-374-300-18400	7	Sequence 18400, A
1105	73	3.3	609	US-11-374-300-17528	7	Sequence 17528, A
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1108	73	3.3	629	US-11-374-300-10563	7	Sequence 10563, A
1109	73	3.3	630	US-11-374-300-40932	7	Sequence 40932, A
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1113	73	3.3	729	US-11-374-300-2568	7	Sequence 2568, Ap
1114	73	3.3	745	US-11-374-300-17135	7	Sequence 17135, A
1115	73	3.3	750	US-11-816-601-211	7	Sequence 211, APP
1116	73	3.3	787	US-11-374-300-37326	7	Sequence 37326, A
1117	73	3.3	819	US-11-374-300-17346	7	Sequence 17346, A
1118	73	3.3	895	US-11-374-300-12320	7	Sequence 12320, A
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1121	3.3	73	1083	7	US-11-374-300-22076	Sequence 22076, A
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1125	3.3	73	1275	7	US-11-374-300-43755	Sequence 43755, A
1126	3.3	73	1383	7	US-11-838-500-82	Sequence 82, Appl
1127	3.3	73	1383	7	US-11-838-500-86	Sequence 86, Appl
1128	3.3	73	1383	7	US-11-838-500-87	Sequence 87, Appl
1129	3.3	73	1389	7	US-11-838-500-79	Sequence 79, Appl
1130	3.3	73	1955	7	US-11-374-300-29533	Sequence 29533, A
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1143	3.3	72.5	421	1	PCT-US07-18368A-24318	Sequence 24318, A
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1148	3.3	72.5	486	7	US-11-816-233-137	Sequence 137, App
1149	3.3	72.5	486	7	US-11-816-233-140	Sequence 140, App
1150	3.3	72.5	486	7	US-11-816-233-141	Sequence 141, App
1151	3.3	72.5	486	7	US-11-816-233-142	Sequence 142, App
1152	3.3	72.5	486	7	US-11-816-233-143	Sequence 143, App
1153	3.3	72.5	486	7	US-11-816-233-144	Sequence 144, App
1154	3.3	72.5	486	7	US-11-816-233-145	Sequence 145, App
1155	3.3	72.5	486	7	US-11-816-233-146	Sequence 146, App
1156	3.3	72.5	486	7	US-11-816-233-147	Sequence 147, App
1157	3.3	72.5	486	7	US-11-816-233-148	Sequence 148, App
1158	3.3	72.5	486	7	US-11-816-233-149	Sequence 149, App
1159	3.3	72.5	493	7	US-11-374-300-22836	Sequence 22836, A
1160	3.3	72.5	510	7	US-11-374-300-18983	Sequence 18983, A
1161	3.3	72.5	524	7	US-11-374-300-37875	Sequence 37875, A
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1171	3.3	72.5	652	1	PCT-US07-18368A-44027	Sequence 44027, A
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1175	3.3	72.5	708	7	US-11-374-300-46821	Sequence 46821, A
1176	3.3	72.5	756	7	US-11-781-665-4642	Sequence 4642, Ap
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1178	3.3	72.5	817	7	US-11-374-300-30510	Sequence 30510, A
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1186	3.3	72.5	961	7	US-11-374-300-28031	Sequence 28031, A
1187	3.3	72.5	974	7	US-11-374-300-9503	Sequence 9503, Ap
1188	3.3	72.5	1021	7	US-11-374-300-2655	Sequence 2655, Ap
1189	3.3	72.5	1030	1	PCT-US07-13803-776	Sequence 776, App
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1196	1650	72.5	3.3	US-11-374-300-22485	Sequence 22485, A
1197	2224	72.5	3.3	US-11-880-377-2476	Sequence 2476, Ap
1198	3734	72.5	3.3	US-11-374-300-25110	Sequence 25110, A
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1203	283	72	3.3	US-11-374-300-31687	Sequence 31687, A
1204	306	72	3.3	PCT-US07-02698-35	Sequence 35, Appl
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1206	306	72	3.3	PCT-US07-18368A-26151	Sequence 26151, A
1207	311	72	3.3	US-11-374-300-39035	Sequence 39035, A
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1210	338	72	3.3	US-11-374-300-35597	Sequence 35597, A
1211	377	72	3.3	US-11-374-300-16623	Sequence 16623, A
1212	390	72	3.3	US-11-374-300-28044	Sequence 28044, A
1213	390	72	3.3	US-11-374-300-47777	Sequence 47777, A
1214	393	72	3.3	US-11-374-300-47961	Sequence 47961, A
1215	402	72	3.3	US-11-833-720-95	Sequence 95, Appl
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1217	402	72	3.3	US-11-884-899-95	Sequence 95, Appl
1218	402	72	3.3	US-11-817-937-54	Sequence 54, Appl
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1222	464	72	3.3	PCT-US07-18368A-8150	Sequence 8150, Ap
1223	523	72	3.3	PCT-US07-76899-33	Sequence 33, Appl
1224	523	72	3.3	PCT-US07-76892-33	Sequence 33, Appl
1225	525	72	3.3	US-11-374-300-39956	Sequence 39956, A
1226	540	72	3.3	PCT-US07-18368A-24472	Sequence 24472, A
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1228	544	72	3.3	US-11-374-300-25537	Sequence 25537, A
1229	547	72	3.3	US-11-374-300-38575	Sequence 38575, A
1230	563	72	3.3	US-11-374-300-43230	Sequence 43230, A
1231	585	72	3.3	US-11-374-300-20508	Sequence 20508, A
1232	585	72	3.3	US-11-374-300-18579	Sequence 18579, A
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1237	620	72	3.3	US-11-374-300-47093	Sequence 47093, A
1238	663	72	3.3	US-11-374-300-41716	Sequence 41716, A
1239	664	72	3.3	US-11-374-300-21195	Sequence 21195, A
1240	670	72	3.3	US-11-781-665-3987	Sequence 3987, Ap
1241	681	72	3.3	US-11-374-300-34445	Sequence 34445, A
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1263	1022	72	3.3	PCT-US07-18368A-1936	Sequence 1936, Ap
1264	1022	72	3.3	US-11-374-300-2564	Sequence 2564, Ap
1265	1032	72	3.3	PCT-US07-18368A-12375	Sequence 12375, A
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1270	72	3.3	1207	7	US-11-781-818-16	Sequence 16, Appl
1271	72	3.3	1256	7	PCT-US07-13803-651	Sequence 651, App
1272	72	3.3	1301	1	PCT-US07-18368A-19801	Sequence 19801, A
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1275	72	3.3	1391	1	US-11-490-374A-1076	Sequence 1076, Ap
1276	72	3.3	1391	1	US-11-490-374A-1077	Sequence 1077, Ap
1277	72	3.3	1391	1	US-11-490-374A-1078	Sequence 1078, Ap
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1283	71.5	3.2	318	7	US-11-374-300-19770	Sequence 19770, A
1284	71.5	3.2	348	1	US-11-374-300-10073	Sequence 10073, A
1285	71.5	3.2	362	1	US-11-490-374A-537	Sequence 537, App
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1287	71.5	3.2	374	7	US-11-374-300-10124	Sequence 10124, A
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1289	71.5	3.2	390	1	US-11-374-300-38208	Sequence 38208, A
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1294	71.5	3.2	407	7	US-11-374-300-20843	Sequence 20843, A
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1305	71.5	3.2	493	7	US-11-374-300-20034	Sequence 20034, A
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1497	70.5	3.2	998	8	US-60-911-843A-18	Sequence 18, Appl
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Job time : 44 secs

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

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         2: pir2:*
         3: pir3:*
         4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	174.5	7.9	825	2	T29634	hypothetical prote
2	160.5	7.3	477	2	S53362	mucin 5AC (clone J
3	155.5	7.0	770	2	T22808	hypothetical prote
4	154.5	7.0	851	2	T22696	hypothetical prote
5	154	7.0	534	2	T39903	serine-rich protei
6	151.5	6.9	1251	2	T21389	hypothetical prote
7	150.5	6.8	797	1	VGBEX1	glycoprotein X pre
8	150.5	6.8	860	2	JC4566	chitinase (EC 3.2.
9	149.5	6.8	3020	2	A43932	mucin 2 precursor,
10	149.5	6.8	3570	2	T45025	mucin MUC5B, trach
11	147.5	6.7	790	2	T34293	hypothetical prote
12	147.5	6.7	1609	2	S25345	probable membrane
13	147	6.6	662	2	A45155	mucin FIM-C.1 - Af
14	146	6.6	786	1	A47547	serine proteinease
15	144.5	6.5	505	2	B46629	mucin 6, gastric (
16	144.5	6.5	1104	2	S59310	probable membrane
17	143	6.5	626	2	S53871	Pmel 17 protein -
18	142.5	6.4	377	2	A48018	mucin 7 precursor,
19	142.5	6.4	491	2	A49179	melanoma antigen h
20	142.5	6.4	866	2	T45462	membrane glycoprot
21	142.5	6.4	867	2	T45463	membrane glycoprot
22	142.5	6.4	1161	2	S57180	probable membrane
23	141	6.4	1777	2	T34369	hypothetical prote
24	141	6.3	292	2	S24169	mucin - rat
25	140	6.3	1275	2	T33369	hypothetical prote
26	138	6.2	909	1	QRXLL2	LDL receptor 2 pre
27	137.5	6.2	1630	2	A53577	ascites sialoglyco
28	137	6.2	528	2	I47141	gastric mucin (clo
29	136.5	6.2	1229	2	T25697	hypothetical prote
30	136	6.2	503	2	S63257	probable membrane
31	136	6.2	796	2	T21460	hypothetical prote
32	135.5	6.1	322	2	A53715	apomucin precursor
33	135.5	6.1	543	2	S35047	mucin JUL7 - human
34	135.5	6.1	1299	2	T47182	hypothetical prote
35	135.5	6.1	2271	2	F90073	hypothetical prote
36	134	6.1	164	2	I53641	mucin 5AC - human
37	133.5	6.0	708	2	T19474	hypothetical prote
38	133.5	6.0	3507	2	T34513	hypothetical prote
39	133	6.0	556	2	S51892	probable membrane
40	133	6.0	610	2	S35049	mucin JER57 - huma
41	133	6.0	636	2	S63131	probable membrane
42	133	6.0	1075	2	S48992	flocculation prote
43	133	6.0	1367	2	S51959	hypothetical prote
44	132	6.0	1162	2	JH0557	exo-alpha-sialidas
45	131	5.9	725	2	A41258	a-agglutinin core
46	130.5	5.9	631	2	I52257	episialin - mouse
47	129.5	5.9	400	2	A28172	spasmolysin precur
48	129.5	5.9	1032	2	T34433	hypothetical prote
49	129.5	5.9	1367	1	S48478	glucan 1,4-alpha-g
50	129.5	5.9	2232	2	T34434	hypothetical prote
51	129	5.8	279	2	S53363	mucin 5AC (clone J
52	129	5.8	739	2	T21769	hypothetical prote
53	128.5	5.8	234	1	QQBE43	membrane antigen g
54	128	5.8	214	2	A46629	mucin 6, gastric (
55	128	5.8	605	2	S48940	hypothetical prote
56	128	5.8	693	2	T19551	mucin-like protein
57	128	5.8	709	2	T28712	hypothetical prote
58	128	5.8	870	2	S74291	hypothetical prote
59	127.5	5.8	559	2	B56731	chromatin assembly
60	127.5	5.8	798	2	T34248	hypothetical prote
61	127.5	5.8	1851	2	T19964	hypothetical prote
62	127	5.7	1260	2	S60896	agglutinin-like pr
63	126.5	5.7	327	2	S20074	promastigote surfa
64	126.5	5.7	354	2	T46740	microfilarial shea
65	126.5	5.7	371	2	S20075	promastigote surfa
66	126.5	5.7	1832	2	T31113	mucin-like glycopr
67	126.5	5.7	2225	2	T26063	syndecan-3 - chick
68	126	5.7	384	2	A44146	mucin (clone PGM-2
69	125.5	5.7	317	2	S55316	LDL receptor 1 pre
70	125.5	5.7	620	2	A70525	mucin like protein
71	125.5	5.7	909	1	QRXLL1	spore coat protein
72	125	5.7	235	2	PC2022	cellular hepatitis
73	125	5.7	600	2	S07638	hypothetical prote
74	124.5	5.6	451	2	S71754	hypothetical prote
75	124.5	5.6	645	2	T29818	MSB2 protein - yea
76	124.5	5.6	1127	2	T25804	otogelin - mouse
77	124.5	5.6	1306	2	S25370	hypothetical prote
78	124.5	5.6	2910	2	T42214	hypothetical prote
79	124	5.6	896	2	T22061	hypothetical prote
80	124	5.6	948	2	T11678	hypothetical prote
81	124	5.6	1224	2	S28368	mucin 2, intestina
82	124	5.6	1374	2	S69875	hypothetical prote
83	124	5.6	1513	2	A54895	probable membrane
84	124	5.6	1681	2	S59693	probable membrane
85	124	5.6	1859	2	S63325	hypothetical prote
86	124	5.6	1859	2	S64633	tumor-associated m
87	123.5	5.6	786	2	T16509	chitinase (EC 3.2.
88	123	5.6	630	2	A39344	probable extracell
89	123	5.6	660	2	JW0067	probable membrane
90	123	5.6	1067	2	D75625	Na+/Ca2+-exchan
91	122.5	5.5	542	2	S64030	secreted acid phos
92	122	5.5	1199	2	S20969	probable membrane
93	121.5	5.5	888	2	T46726	cell wall surface
94	121.5	5.5	1041	2	S55862	mucin - rhesus mac
95	121.5	5.5	4776	2	E95206	hypothetical prote
96	121	5.5	216	2	I51920	hypothetical prote
97	121	5.5	402	2	E86185	hypothetical prote
98	121	5.5	520	2	A71564	probable membrane
99	121	5.5	1382	2	S70310	hypothetical prote
100	121	5.5	1796	2	S65004	probable membrane
101	121	5.5	1829	2	T24583	hypothetical prote
102	120.5	5.5	560	2	T32661	hypothetical prote

No.	Len	pI	MW	Accession	N	Description
103	767	5.5	120.5	JU0474	1	glucan 1,4-alpha-g
104	778	5.5	120.5	ALBYG	1	glucan 1,4-alpha-g
105	1169	5.5	120.5	S38181	2	flocculation prote
106	273	5.4	120	T44657	2	protein GP80 [impo
107	395	5.4	120	I52842	2	CD43 Lp-3 antigen
108	395	5.4	120	A43545	2	leukosialin CD43 p
109	575	5.4	120	T21775	2	hypothetical prote
110	750	5.4	120	T42614	2	probable envelope
111	349	5.4	119.5	T42965	2	glycoprotein - ate
112	573	5.4	119.5	A33533	2	cell surface glyco
113	1205	5.4	119.5	S64819	2	probable membrane
114	610	5.4	119	PN0012	2	mucin 4, tracheal
115	996	5.4	119	JE0237	2	apolipoprotein E r
116	232	5.4	118.5	A60095	2	larval glue protei
117	294	5.4	118.5	A37232	2	mucin, tracheal (A
118	507	5.4	118.5	T44768	2	antifreeze glycope
119	995	5.4	118.5	S50358	2	hypothetical prote
120	1118	5.4	118.5	A48292	2	mucin, tracheobron
121	1532	5.4	118.5	A61262	2	collagen alpha 1(X
122	496	5.3	118	E90181	2	hypothetical prote
123	789	5.3	118	I59550	2	aryl hydrocarbon r
124	886	5.3	118	S29605	2	glycoprotein 350/2
125	977	5.3	118	T16232	2	hypothetical prote
126	230	5.3	117.5	T33564	2	hypothetical prote
127	907	5.3	117.5	QQBE21	1	membrane antigen g
128	1032	5.3	117.5	S65341	2	probable membrane
129	1541	5.3	117.5	S46686	2	hypothetical prote
130	518	5.3	117	T49778	2	hypothetical prote
131	551	5.3	117	S64314	2	probable membrane
132	567	5.3	117	A70603	2	hypothetical prote
133	592	5.3	117	T34446	2	hypothetical prote
134	700	5.3	117	A54641	2	interspersed repea
135	621	5.3	116.5	T20307	2	hypothetical prote
136	623	5.3	116.5	F75523	2	osteoblast specifi
137	672	5.3	116.5	T20310	2	hypothetical prote
138	3421	5.3	116.5	WZBBB6	1	367K tegument prot
139	168	5.2	116	S52994	2	arabinogalactan-li
140	368	5.2	116	S67387	2	hypothetical prote
141	624	5.2	116	S49000	2	hypothetical prote
142	695	5.2	116	T39954	2	probable gtpase ac
143	722	5.2	116	T22359	2	hypothetical prote
144	877	5.2	116	A25962	2	mitosis inhibitor
145	1199	5.2	116	A40670	2	nuclear envelope p
146	1237	5.2	116	A34598	2	ecdysone-induced p
147	1247	5.2	115.5	T42209	2	neural plakophilin
148	1394	5.2	116	B34598	2	ecdysone-induced p
149	299	5.2	115.5	G70784	2	probable mmp53 pro
150	310	5.2	115.5	YA2Q31	1	300K antigen Ag231
151	516	5.2	115.5	A44494	2	cAMP-responsive el
152	625	5.2	115.5	T20634	2	hypothetical prote
153	639	5.2	115.5	T43190	2	probable actin-bin
154	690	5.2	115.5	T31597	1	protein W10G1.5 [
155	400	5.2	114.5	A39822	2	leukosialin precur
156	419	5.2	115	T04530	2	hypothetical prote
157	419	5.2	115	D85334	2	hypothetical prote
158	463	5.2	115	T38444	2	hypothetical prote
159	921	5.1	115	AE0332	1	conserved hypothet
160	1217	5.2	114.5	T25894	2	hypothetical prote
161	1603	5.2	114.5	S17983	2	gene posterior sex
162	293	5.2	114	G87018	1	probable membrane
163	507	5.2	114	S64507	2	mucin 3 - human (f
164	510	5.2	114	H84824	1	En/Spm-like transp
165	543	5.2	114	A41285	2	interleukin enhanc
166	1547	5.2	114	T28657	2	blackjack protein,
167	354	5.1	113.5	S59521	2	mucin 5ac - mouse
168	373	5.1	113.5	S43455	2	hypothetical prote
169	543	5.1	113.5	A41221	2	early growth respo
170	548	5.1	113.5	E70546	2	hypothetical prote
171	627	5.1	113.5	T27123	2	hypothetical prote
172	1589	5.1	113.5	T13606	2	hypothetical prote
173	307	5.1	113	GSFF3	1	salivary glue prot
174	522	5.1	113	S41819	2	nucleoporin p62 -
175	1537	5.1	113	S53465	2	flocculation prote
176	2090	5.1	113	S26058	2	probable transform
177	1072	5.1	112.5	A86827	2	hypothetical prote
178	353	5.1	112	A41558	2	N-syndecan - rat (
179	359	5.1	112	S42787	2	serine/threonine-r
180	1043	5.1	112	T13172	2	gag-like protein p
181	1180	5.1	112	E86719	2	hypothetical prote
182	1231	5.1	112	T18532	2	serine/threone pr
183	1277	5.1	112	S70306	2	hypothetical prote
184	1348	5.1	112	S27812	2	probable epidermal
185	1419	5.1	112	T30531	2	agglutinin-like ad
186	2251	5.1	112	T24490	2	hypothetical prote
187	670	5.1	111.5	F36791	2	hypothetical prote
188	1186	5.0	111.5	S72229	2	meiotic recombinat
189	1235	5.0	111.5	T13710	2	protein-tyrosine k
190	1804	5.0	111.5	H96597	2	hypothetical prote
191	462	5.0	111	F75588	2	probable kynurenin
192	962	5.0	111	T22459	2	hypothetical prote
193	1230	5.0	111	T22458	2	hypothetical prote
194	2761	5.0	111	T21064	2	hypothetical prote
195	370	5.0	110.5	T32615	2	transcription fact
196	416	5.0	110.5	A55237	2	transcription fact
197	510	5.0	110.5	A45338	2	connexin-56 - chic
198	561	5.0	110.5	T14792	2	hypothetical prote
199	623	5.0	110	A48123	2	cell cycle regulat
200	785	5.0	110	T51203	2	related to ser/thr
201	1224	5.0	110	T14007	2	microtubule-associ
202	3968	5.0	110	A44265	2	trithorax homolog
203	5327	5.0	110	T13564	2	microtubule-associ
204	167	5.0	109.5	A33532	2	mucin SMUC-40 - hu
205	637	5.0	109.5	C43273	2	heregulin precurso
206	832	5.0	109.5	JC8051	2	protein tyrosine p
207	1335	5.0	109.5	T18289	2	racGAP protein - s
208	1758	5.0	109.5	S57015	2	probable purine nu
209	3191	5.0	109.5	T22945	2	hypothetical prote
210	319	4.9	109	T43040	2	hypothetical prote
211	369	4.9	109	AG1950	2	hypothetical prote
212	413	4.9	109	A55238	2	transcription fact
213	528	4.9	109	S69589	2	hypothetical prote
214	542	4.9	109	I39540	2	chitinase (EC 3.2.
215	668	4.9	109	A41234	2	melanocyte-specifi
216	753	4.9	109	T24869	2	hypothetical prote
217	1088	4.9	109	IJXLNL	2	neural cell adhesi
218	1254	4.9	109	T18277	1	kinesin heavy chai
219	1273	4.9	109	S58782	2	SEC31 protein - ye
220	263	4.9	108.5	T38003	2	hypothetical ser-t
221	518	4.9	108.5	F75460	2	hypothetical prote
222	766	4.9	108.5	A47001	2	transcription fact
223	796	4.9	108.5	E96654	2	hypothetical prote
224	898	4.9	108.5	T14764	2	hypothetical prote
225	1367	4.9	108.5	T33819	2	hypothetical prote
226	205	4.9	108.5	S55670	2	hypothetical prote
227	345	4.9	108	B88103	2	transcription fact
228	457	4.9	108	I54340	2	hypothetical prote
229	598	4.9	108	T22610	2	leukosialin precur
230	651	4.9	108	T16450	2	hypothetical prote
231	662	4.9	108	I38400	2	hypothetical prote
232	1076	4.9	108	C96620	2	conserved hypothet
233	383	4.9	107.5	T46707	2	hypothetical prote
234	475	4.9	107.5	S49886	2	gene posterior sex
235	514	4.8	107.5	A31643	2	probable membrane
236	648	4.8	107.5	PC4395	2	mucin 3 - human (f
237	713	4.9	107.5	JN0133	2	WD-40 repeat regul
238	760	4.9	107.5	S07896	1	transcription fact
239	1348	4.9	107.5	A43917	2	probable epidermal
240	2130	4.9	107.5	AB0821	2	probable exported
241	2414	4.9	107.5	A54277	2	transcription adap
242	347	4.8	107	S10571	2	mucin 1 precursor,
243	1286	4.8	107	A88396	2	protein M01E10.2 [
244	263	4.8	106.5	S01360	2	salivary glue prot
245	298	4.8	106.5	S01179	2	hypothetical prote
246	338	4.8	106.5	S28004	2	hypothetical prote
247	378	4.8	106.5	S61992	2	probable cell surf
248	434	4.8	106.5	B84684	2	SLG1 protein - yea

No.	MW	pI	Length	N	Accession	Description
249	106.5	4.8	609	2	S62518	hypothetical prote
250	106.5	4.8	647	2	S26386	transcription fact
251	106.5	4.8	1791	2	T02345	hypothetical prote
252	106.5	4.8	1952	2	T48814	hypothetical prote
253	106	4.8	303	2	T42703	hypothetical prote
254	106	4.8	514	2	A44100	cell adhesion mole
255	106	4.8	931	2	T49710	related to glucan
256	106	4.8	980	1	T05414	protein kinase hom
257	106	4.8	1018	2	S44758	C14B9.6 protein -
258	106	4.8	1151	2	T18535	high molecular mas
259	106	4.8	1282	2	JE0120	glycoprotein A - m
260	106	4.8	1849	2	C41859	IgA-specific metal
261	105.5	4.8	547	2	B56573	nuclear pore compl
262	105.5	4.8	584	2	B25682	homeotic protein E
263	105.5	4.8	645	2	B43273	heregulin, splice
264	105.5	4.8	710	1	QQBE22	membrane antigen g
265	105.5	4.8	810	2	D86818	hypothetical prote
266	105.5	4.8	871	2	T43427	pob1 protein - fis
267	105.5	4.8	1092	1	JN0635	neural cell adhesi
268	105.5	4.8	2187	2	T30826	nascent polypeptid
269	105	4.7	246	2	PC4397	mucin 3 T10 - huma
270	105	4.7	487	2	S61993	probable membrane
271	105	4.7	515	2	A42140	box B-binding fact
272	105	4.7	538	2	S65764	chitinase (EC 3.2.
273	105	4.7	903	2	T19209	probable protein k
274	105	4.7	936	2	S64384	probable membrane
275	105	4.7	1262	2	T25168	hypothetical prote
276	105	4.7	1459	2	T30196	kinesin motor prot
277	105	4.7	1459	2	T32271	hypothetical prote
278	105	4.7	1469	2	T09219	basal transcriptio
279	105	4.7	2109	1	I50421	aggrecan precursor
280	104.5	4.7	415	2	B82588	rare lipoprotein A
281	104.5	4.7	591	2	T25636	hypothetical prote
282	104.5	4.7	636	2	T38473	probable serine/th
283	104.5	4.7	795	2	T20609	hypothetical prote
284	104.5	4.7	833	2	E90577	lipoprotein vsaC [
285	104.5	4.7	990	2	I51618	nucleolar phosphop
286	104.5	4.7	1129	2	T25635	hypothetical prote
287	104.5	4.7	1175	2	T25634	hypothetical prote
288	104.5	4.7	1212	2	T13804	shs protein - frui
289	104.5	4.7	1578	2	I48216	neurexin III-alpha
290	104.5	4.7	1779	2	T31085	xylanase - Caldice
291	104.5	4.7	2397	1	A55535	versican precursor
292	104	4.7	456	2	T38221	hypothetical serin
293	104	4.7	583	2	S67571	hypothetical prote
294	104	4.7	879	2	S23006	shed acute-phase a
295	104	4.7	1012	1	I53172	RAB-28 - mouse
296	104	4.7	1344	1	A35175	mucin 1 precursor,
297	103.5	4.7	244	1	T12458	hypothetical prote
298	103.5	4.7	262	2	T33597	hypothetical prote
299	103.5	4.7	416	2	S09761	hypothetical prote
300	103.5	4.7	448	2	S17370	DNA-binding protei
301	103.5	4.7	491	2	C46230	RNA-binding protei
302	103.5	4.7	570	2	AD0223	flagellar M-ring p
303	103.5	4.7	630	2	T00352	hypothetical prote
304	103.5	4.7	658	2	T41309	hypothetical threo
305	103.5	4.7	792	2	S70305	hypothetical prote
306	103.5	4.7	954	2	E86174	protein F19P19.26
307	103.5	4.7	959	2	S35061	protovillin - slim
308	103.5	4.7	1163	2	A36685	205K microtubule-a
309	103.5	4.7	1224	2	T40765	web1 protein homol
310	103.5	4.7	1247	2	T45743	hypothetical prote
311	103.5	4.7	1571	2	T00062	hypothetical prote
312	103.5	4.7	2282	2	T47717	DNA-binding protei
313	103.5	4.7	2440	2	S39162	transcription coac
314	103	4.7	202	2	AB2378	hypothetical prote
315	103	4.7	369	2	G83434	translocation prot
316	103	4.7	378	2	S00842	leukosialin precur
317	103	4.7	394	2	T20633	syndecan precursor
318	103	4.7	395	2	A54949	mucin - rat (fragm
319	103	4.7	447	2	A39321	spore germination
320	103	4.7	532	2	B35621	developmental cont
321	103	4.7	533	2	JS0304	

No.	MW	pI	Length	N	Accession	Description
322	103	4.7	536	2	T37544	hypothetical serin
323	103	4.7	625	2	T50992	hypothetical prote
324	103	4.7	636	2	I61718	neu differentiatio
325	103	4.7	851	2	AD1427	internalin, probab
326	103	4.7	937	2	S58135	hyphally regulated
327	103	4.7	961	2	AE0375	probable cation-tr
328	103	4.7	1117	2	S38673	desmoglein 2 - hum
329	103	4.7	1733	1	RNBY2L	DNA-directed RNA p
330	102.5	4.6	186	2	B70595	hypothetical prote
331	102.5	4.6	329	2	S38082	pathogenesis-relat
332	102.5	4.6	588	2	JC8021	chitinase (EC 3.2.
333	102.5	4.6	640	2	A43273	heregulin precurso
334	102.5	4.6	741	2	T40095	Zinc finger, C3HC4
335	102.5	4.6	1443	2	S05979	steroid hormone re
336	102.5	4.6	1802	2	S69703	HKR1 protein precu
337	102.5	4.6	2180	2	A47651	zinc-finger protei
338	102	4.6	180	2	T31974	hypothetical prote
339	102	4.6	337	2	C65028	hypothetical 36.2K
340	102	4.6	482	2	AG1147	P60 extracellular
341	102	4.6	484	2	A41487	protein P60 precur
342	102	4.6	671	2	A38109	autolysin - Entero
343	102	4.6	683	2	T03146	probable glycoprot
344	102	4.6	754	2	A56619	female sterile hom
345	102	4.6	803	2	T40475	bromodomain prote
346	102	4.6	1131	2	T41144	hypothetical serin
347	102	4.6	1159	2	S62562	probable nuclear p
348	102	4.6	1607	2	T02837	long chain fatty a
349	102	4.6	5376	2	T42215	zonadhesin - mouse
350	101.5	4.6	328	2	S67570	hypothetical prote
351	101.5	4.6	380	2	T28081	hypothetical prote
352	101.5	4.6	389	2	T33340	hypothetical prote
353	101.5	4.6	448	2	A38445	EV12B protein prec
354	101.5	4.6	460	2	T45968	hypothetical prote
355	101.5	4.6	508	2	A32225	nerve growth facto
356	101.5	4.6	525	2	A35596	nuclear pore glyco
357	101.5	4.6	551	2	S52287	urbain - silkworm
358	101.5	4.6	649	2	T24505	hypothetical prote
359	101.5	4.6	1133	2	A54164	sterol regulatory
360	101.5	4.6	1402	2	T17456	cell surface prote
361	101.5	4.6	2338	2	T25810	hypothetical prote
362	101.5	4.6	2359	2	T03094	A-kinase anchor pr
363	101.5	4.6	328	2	A46521	52K phosphoprotein
364	101	4.6	330	2	I57835	lymphocyte-specifi
365	101	4.6	337	2	B91051	probable membrane
366	101	4.6	413	2	S28066	sexual differentia
367	101	4.6	445	2	S06992	wall-associated pr
368	101	4.6	587	2	A60367	transforming prote
369	101	4.6	622	2	S57684	probable membrane
370	101	4.6	626	1	NBHUIA	platelet glycoprot
371	101	4.6	647	2	B34457	204 protein - mous
372	101	4.6	736	2	T41259	hypothetical prote
373	101	4.6	822	2	JC4076	dextranase (EC 3.2
374	101	4.6	861	2	S77409	hypothetical prote
375	101	4.6	927	2	T24031	hypothetical prote
376	101	4.6	928	2	S64350	DNA topoisomerase
377	101	4.6	1016	2	T19006	hypothetical prote
378	101	4.6	1203	2	T17415	ankyrin related pr
379	100.5	4.5	213	2	A86228	mycelial surface a
380	100.5	4.5	217	2	S01358	hypothetical prote
381	100.5	4.5	394	2	T21752	salivary glue prot
382	100.5	4.5	474	2	S65763	chitinase (EC 3.2.
383	100.5	4.5	531	2	T04463	hypothetical prote
384	100.5	4.5	733	2	A45301	microtubule-associ
385	100.5	4.5	735	2	S64504	transcription init
386	100.5	4.5	1015	2	JC6552	DNA topoisomerase
387	100.5	4.5	1208	2	T27822	hypothetical prote
388	100.5	4.5	1262	2	T22523	hypothetical prote
389	100.5	4.5	1357	2	T29265	hypothetical prote
390	100.5	4.5	1611	2	T38236	cellulose-binding
391	100.5	4.5	1848	2	A44140	mucin 3 T9 - human
392	100	4.5	236	2	PC4396	hypothetical prote
393	100	4.5	344	2	S09883	hypothetical zinc
394	100	4.5	442	2	T37733	hypothetical zinc

395	100	4.5	526	T13687	2	hypothetical prote
396	100	4.5	617	T49444	2	lustrin A related
397	100	4.5	791	A56241	2	aryl hydrocarbon r
398	100	4.5	1072	A37127	2	microtubule-associ
399	100	4.5	1301	A41622	1	protein-tyrosine-p
400	100	4.5	1742	S76110	2	hypothetical prote
401	100	4.5	2415	A39086	1	aggrecan precursor
402	100	4.5	3562	A47171	2	chondroitin sulfat
403	99.5	4.5	466	T11684	1	RVS167 protein hom
404	99.5	4.5	520	S62521	2	hypothetical prote
405	99.5	4.5	597	S43743	1	probable dual spec
406	99.5	4.5	639	I61719	2	neu differentiatio
407	99.5	4.5	881	S56032	2	probable membrane
408	99.5	4.5	892	A41697	2	nitrate assimilati
409	99.5	4.5	959	S32016	2	flagellum-associat
410	99.5	4.5	1224	E71611	2	hypothetical prote
411	99.5	4.5	2346	T13829	2	Tpr homolog - frui
412	99.5	4.5	2481	D90011	2	FmtB protein [impo
413	99	4.5	281	F42517	2	A4L protein - vacc
414	99	4.5	333	RPXFIM	1	repetitive protein
415	99	4.5	417	T24618	2	hypothetical prote
416	99	4.5	507	T50398	2	hypothetical serin
417	99	4.5	536	H71563	2	hypothetical prote
418	99	4.5	562	B41035	2	chitinase (EC 3.2.
419	99	4.5	562	S50371	2	chitinase (EC 3.2.
420	99	4.5	627	G66860	2	serine/threonine p
421	99	4.5	646	I30049	2	cell surface glyco
422	99	4.5	696	A29635	2	transcription fact
423	99	4.5	713	B32575	2	C-ski protein FB28
424	99	4.5	770	S30293	1	transcription fact
425	99	4.5	899	T16204	2	hypothetical prote
426	99	4.5	942	T38649	2	hypothetical homeo
427	99	4.5	942	T19553	2	hypothetical prote
428	99	4.5	963	T40290	2	hypothetical prote
429	98.5	4.5	1272	S26180	2	neurofascin - chic
430	98.5	4.5	1297	T30274	2	proteolaisin - se
431	98.5	4.5	1436	T14895	2	DNA helicase 1 - A
432	98.5	4.5	1513	T23681	2	hypothetical prote
433	98.5	4.5	1882	T00069	2	hypothetical prote
434	98.5	4.5	317	T39869	2	probable lysophosp
435	98.5	4.5	385	T38113	2	hypothetical serin
436	98.5	4.5	441	T31482	2	hypothetical prote
437	98.5	4.5	553	T48486	2	hypothetical prote
438	98.5	4.5	678	S54308	2	DNA binding protei
439	98.5	4.5	886	T40734	1	probable adenylate
440	98.5	4.5	917	S51254	2	STE5 protein - yea
441	98.5	4.5	973	T40778	2	hypothetical 129.5
442	98.5	4.5	1005	C71513	2	hypothetical prote
443	98.5	4.5	1006	T42731	2	atrophin-1 related
444	98.5	4.5	1522	T39371	2	transcription regu
445	98.5	4.5	1612	T30805	2	dutt1 protein - mo
446	98.5	4.5	1658	S55101	2	hypothetical prote
447	98.5	4.5	1858	T18273	2	DNA binding protei
448	98.5	4.5	3942	T42730	2	1-phosphatidylinos
449	98	4.4	266	B87498	2	Bassoon protein -
450	98	4.4	379	S50125	2	hypothetical prote
451	98	4.4	380	S05457	2	larval glue protei
452	98	4.4	409	S44346	2	coat protein - Cym
453	98	4.4	440	S51614	2	RAD23 protein homo
454	98	4.4	532	T49467	2	Algal-CAM - Volvox
455	98	4.4	621	T24090	2	related to COP1-in
456	98	4.4	802	T21315	2	hypothetical prote
457	98	4.4	817	T22442	2	hypothetical prote
458	98	4.4	895	I54343	2	dystroglycan - hum
459	98	4.4	904	T22457	2	hypothetical prote
460	98	4.4	943	S28400	2	gag-like protein -
461	98	4.4	989	T47503	2	hypothetical prote
462	98	4.4	1007	H81670	2	conserved hypothet
463	98	4.4	1091	IJCHNL	1	neural cell adhesi
464	98	4.4	1114	I50222	2	deltaEF1 - chicken
465	98	4.4	1428	AC2224	2	hypothetical prote
466	98	4.4	1737	A59235	2	unconventional myo
467	98	4.4	1844	S01956	2	hypothetical prote

468	98	4.4	2157	S71461	2	proline-rich prote
469	98	4.4	3092	S46009	2	GTPase-activating
470	98	4.4	3624	AD0835	2	large repetitive p
471	97.5	4.4	284	T42367	2	a-agglutinin core
472	97.5	4.4	516	PQ0553	2	polyprotein - plum
473	97.5	4.4	601	T37738	2	hypothetical prote
474	97.5	4.4	614	S58306	2	WD-40 repeat regul
475	97.5	4.4	779	S40382	1	box A-binding fact
476	97.5	4.4	839	P75518	2	hypothetical prote
477	97.5	4.4	850	S56015	2	gastric mucin MUC5
478	97.5	4.4	1003	JH0823	2	FL-160-2 protein -
479	97.5	4.4	1076	A35622	1	nuclear pore prote
480	97.5	4.4	1080	S48944	2	hypothetical prote
481	97.5	4.4	1142	C97080	2	levanase/invertase
482	97.5	4.4	1193	B96943	2	2,3-cyclic-nucleot
483	97.5	4.4	1272	T30248	2	fragile X mental r
484	97.5	4.4	1284	T13168	2	probable potassium
485	97.5	4.4	1324	S52863	2	DNA-binding protei
486	97.5	4.4	1474	F69009	2	probable membrane
487	97.5	4.4	1544	T29482	2	hypothetical prote
488	97.5	4.4	1679	S49802	2	probable membrane
489	97.5	4.4	1842	T43409	2	probable fatty-aci
490	97.5	4.4	1842	T38781	2	fatty acid synthas
491	97.5	4.4	1890	T04556	2	hypothetical prote
492	97	4.4	138	D96715	2	protein F4N2.10 [i
493	97	4.4	349	T41394	2	hypothetical serin
494	97	4.4	376	S52137	2	MID2 protein - yea
495	97	4.4	431	S46594	2	probable transcrip
496	97	4.4	448	G88639	2	protein C34H4.2 [i
497	97	4.4	497	B42827	2	interleukin enhanc
498	97	4.4	499	AI1107	2	internalin E [impo
499	97	4.4	511	I50114	2	early growth respo
500	97	4.4	580	T43481	2	probable mucin DXF
501	97	4.4	615	S24761	2	Cpo 61.1 protein -
502	97	4.4	647	T39141	2	hypothetical prote
503	97	4.4	680	A97331	2	membrane associate
504	97	4.4	699	C43674	2	US4 protein - huma
505	97	4.4	739	I56187	2	transcription fact
506	97	4.4	862	S53913	2	FKH2 protein - yea
507	97	4.4	1136	T26953	2	hypothetical prote
508	97	4.4	1985	S19151	2	hypothetical prote
509	97	4.4	2140	T18543	2	probable cell-adhe
510	97	4.4	2529	B64635	2	toxin-like outer m
511	97	4.4	2756	T30183	2	collagen alpha 3(V
512	97	4.4	3176	CGHU3A	1	collagen alpha 3(V
513	96.5	4.4	281	QQVZA5	2	A5L protein - vacc
514	96.5	4.4	303	T02606	2	hypothetical prote
515	96.5	4.4	313	T39212	2	hypothetical prote
516	96.5	4.4	322	B84635	2	hypothetical prote
517	96.5	4.4	345	AH0336	2	probable flagellar
518	96.5	4.4	416	D84657	2	probable SF16 prot
519	96.5	4.4	419	T36894	2	hypothetical prote
520	96.5	4.4	458	T31631	2	calmodulin-binding
521	96.5	4.4	504	I56542	2	hypothetical prote
522	96.5	4.4	560	AB2220	2	probable nucleopor
523	96.5	4.4	598	T38403	2	neu differentiatio
524	96.5	4.4	662	I61722	2	hypothetical prote
525	96.5	4.4	667	T15710	2	hypothetical prote
526	96.5	4.4	680	T19939	2	probable flagellar
527	96.5	4.4	704	S21911	2	BRcore-NS-Z3 prot
528	96.5	4.4	738	T44194	2	hypothetical prote
529	96.5	4.4	738	T44007	2	hypothetical prote
530	96.5	4.4	836	S49940	2	cell division cont
531	96.5	4.4	892	H71558	2	probable translati
532	96.5	4.4	897	S50550	2	SIN1-associated pr
533	96.5	4.4	915	T09550	2	smoothelin - human
534	96.5	4.4	982	A53253	2	microtubule-associ
535	96.5	4.4	1007	T24643	2	hypothetical prote
536	96.5	4.4	1038	H90053	2	hypothetical prote
537	96.5	4.4	1152	A33183	2	microtubule-associ
538	96.5	4.4	1320	JC5630	2	TCOF1 protein - mo
539	96.5	4.4	1468	A44345	2	nucleoporin - rat
540	96.5	4.4	2606	T03159	2	large tegument pro

Seq	Ratio	%	Length	N	Accession	Description
541	4.4	96.5	3147	2	T21328	hypothetical prote
542	4.3	96	62	2	S53366	mucin 5AC (clone M
543	4.3	96	382	1	SUBSN	subtilisin (EC 3.4
544	4.3	96	420	2	A71327	probable protein-e
545	4.3	96	446	2	T45525	WSC4 homolog [impo
546	4.3	96	619	2	T15969	hypothetical prote
547	4.3	96	743	2	T39361	hypothetical prote
548	4.3	96	796	2	T20393	hypothetical prote
549	4.3	96	819	1	S40400	protein kinase SWB
550	4.3	96	822	2	A38420	antifreeze glycopr
551	4.3	96	966	2	S25365	CYC8 protein - yea
552	4.3	96	967	2	S66852	hypothetical protei
553	4.3	96	990	2	H88733	protein F32E10.3 [
554	4.3	96	1026	2	A40315	maternal effect pr
555	4.3	96	1045	2	A39199	endoglucanase B (E
556	4.3	96	1061	2	I49328	retinoblastoma-ass
557	4.3	96	1117	2	S63399	probable membrane
558	4.3	96	1331	2	T49813	related to gastric
559	4.3	96	4063	2	T42993	probable spectrin
560	4.3	96	4101	2	T23530	hypothetical prote
561	4.3	95.5	313	2	A34677	secretory pathway
562	4.3	95.5	417	2	JC7092	Psu1 protein - fis
563	4.3	95.5	526	2	A56573	nuclear pore compl
564	4.3	95.5	552	2	A41035	chitinase (EC 3.2.
565	4.3	95.5	582	2	ERADF2	fiber protein - hu
566	4.3	95.5	630	2	S37884	finger protein MSN
567	4.3	95.5	635	2	F75477	hypothetical prote
568	4.3	95.5	647	2	S00644	protein kinase raf
569	4.3	95.5	693	2	D90441	ABC transporter, p
570	4.3	95.5	839	2	S32158	DNA topoisomerase
571	4.3	95.5	906	2	G90281	conserved hypothet
572	4.3	95.5	925	2	S48768	regulatory protein
573	4.3	95.5	982	2	T18576	serine-threonine k
574	4.3	95.5	1051	1	JW0051	serine/threonine-s
575	4.3	95.5	1174	2	T49868	related to suppres
576	4.3	95.5	1201	2	T29329	hypothetical prote
577	4.3	95.5	1234	2	T31623	hypothetical prote
578	4.3	95.5	1237	2	A54080	protein-tyrosine-p
579	4.3	95.5	3938	2	T42761	Bassoon protein -
580	4.3	95	171	2	F70732	probable lipoprote
581	4.3	95	303	2	S40973	hypothetical prote
582	4.3	95	342	2	T46909	hypothetical prote
583	4.3	95	380	2	VCVGCR	coat protein - Cym
584	4.3	95	390	2	QQBE77	glycoprotein I pre
585	4.3	95	427	2	T29376	hypothetical prote
586	4.3	95	482	2	F71461	hypothetical prote
587	4.3	95	531	2	T22021	hypothetical prote
588	4.3	95	605	2	S71630	metalloproteinase
589	4.3	95	641	2	PH1919	FL-160-4 protein -
590	4.3	95	677	2	T39590	hypothetical prote
591	4.3	95	708	2	T29669	hypothetical prote
592	4.3	95	720	2	A96807	hypothetical prote
593	4.3	95	771	2	S35681	ESG protein - mous
594	4.3	95	837	1	A29512	LDL receptor precu
595	4.3	95	1039	2	S02711	cellulase (EC 3.2.
596	4.3	95	1065	2	S19482	hypothetical prote
597	4.3	95	1109	2	T18536	receptor-like prot
598	4.3	95	1230	2	T18259	probable serine/th
599	4.3	95	1230	2	T18259	serine/threonine p
600	4.3	95	1305	2	AD0428	probable exported
601	4.3	95	1392	2	T51947	probable transcrip
602	4.3	95	1438	2	S59792	probable membrane
603	4.3	95	1438	2	B71610	WD40 WEB-1 homolog
604	4.3	95	1668	2	T13748	sex comb protein -
605	4.3	95	1733	2	S27939	tensin - chicken
606	4.3	95	1792	2	A57075	tensin - chicken (
607	4.3	95	2094	2	S33124	tpr protein - huma
608	4.3	95	2616	2	A57096	nudel protein prec
609	4.3	94.5	245	2	T33363	hypothetical prote
610	4.3	94.5	304	2	T15922	hypothetical prote
611	4.3	94.5	357	2	S27909	hypothetical prote
612	4.3	94.5	388	2	T16861	hypothetical prote
613	4.3	94.5	407	2	I52703	42K membrane glyco
614	4.3	94.5	424	2	T05785	hypothetical prote
615	4.3	94.5	516	2	PQ0552	polyprotein - plum
616	4.3	94.5	533	2	T40011	hypothetical prote
617	4.3	94.5	535	2	S44827	F54F2.2 protein -
618	4.3	94.5	566	2	S54629	hypothetical prote
619	4.3	94.5	587	2	A56015	finger protein SIG
620	4.3	94.5	639	1	WMVQ70	70K protein - pota
621	4.3	94.5	705	2	A35621	spore germination
622	4.3	94.5	813	2	JC5809	hypoxia-inducible
623	4.3	94.5	845	2	T40955	hypothetical prote
624	4.3	94.5	1095	2	T20528	hypothetical prote
625	4.3	94.5	1154	2	S69206	regulator protein
626	4.3	94.5	1350	2	T30341	zinc finger protei
627	4.3	94.5	1496	2	T40016	conserved hypothet
628	4.3	94.5	1634	2	T26517	hypothetical prote
629	4.3	94.5	1702	2	A41859	IgA-specific metal
630	4.3	94.5	2688	2	I49477	alpha-A-crystallin
631	4.3	94.5	3672	2	T23433	hypothetical prote
632	4.3	94.5	3704	2	T37316	probable laminin a
633	4.3	94	108	2	G72708	hypothetical prote
634	4.3	94	194	2	T16382	hypothetical prote
635	4.3	94	210	2	S67140	probable membrane
636	4.3	94	254	2	S48547	probable membrane
637	4.3	94	287	2	S65765	chitinase (EC 3.2.
638	4.3	94	328	2	S01359	salivary glue prot
639	4.3	94	330	2	A30533	lymphocyte-specifi
640	4.3	94	336	2	T31882	hypothetical prote
641	4.3	94	338	2	T04458	hypothetical prote
642	4.3	94	351	2	T32717	hypothetical prote
643	4.3	94	423	2	S74278	hypothetical prote
644	4.3	94	446	2	T19902	hypothetical prote
645	4.3	94	498	2	G97279	protein containing
646	4.3	94	536	2	B46230	RNA-binding protei
647	4.3	94	590	2	S66956	hypothetical prote
648	4.3	94	616	2	A46230	RNA-binding protei
649	4.3	94	623	2	T18892	hypothetical prote
650	4.3	94	644	2	S39356	transcription fact
651	4.3	94	661	2	T24584	hypothetical prote
652	4.3	94	667	2	T00061	hypothetical prote
653	4.3	94	688	2	T23108	hypothetical prote
654	4.3	94	755	2	T20950	hypothetical prote
655	4.3	94	785	2	S54016	SOK2 protein - yea
656	4.3	94	859	2	T29630	hypothetical prote
657	4.3	94	879	1	QRRTLD	LDL receptor precu
658	4.3	94	884	2	T40690	hypothetical prote
659	4.3	94	963	2	T40873	probable transcrip
660	4.3	94	1066	2	G84746	hypothetical prote
661	4.3	94	1184	2	A96638	hypothetical prote
662	4.3	94	1489	2	T31108	cyst germination s
663	4.3	94	1528	2	T37308	ATPase homolog - C
664	4.3	94	1579	2	B91290	probable invasin [
665	4.3	94	1700	2	G86131	probable invasin Z
666	4.3	94	1955	1	AGCH	agrin precursor -
667	4.3	94	2035	2	A40718	host cell factor C
668	4.3	94	2386	1	FNHU	fibronectin precur
669	4.3	94	2845	2	I49505	adenomatous polypo
670	4.3	94	3013	2	AB0480	probable invasin Y
671	4.3	94	4957	2	T03455	ALR protein - huma
672	4.3	94	5262	2	T03454	ALR protein - huma
673	4.3	94	5762	2	A41819	proline-rich pepti
674	4.3	94	6420	2	T30283	polyketide synthas
675	4.2	93.5	214	2	T09854	proline-rich cell
676	4.2	93.5	315	2	T26422	hypothetical prote
677	4.2	93.5	430	2	I48765	mSAP1a - mouse
678	4.2	93.5	453	2	B42093	serum response fac
679	4.2	93.5	474	2	T10271	capsid-associated
680	4.2	93.5	476	2	S28500	hypothetical prote
681	4.2	93.5	510	2	T37541	probable glycolipi
682	4.2	93.5	521	2	F87775	protein C24A11.8 [
683	4.2	93.5	527	2	S64060	probable membrane
684	4.2	93.5	577	2	S72227	finger protein sob
685	4.2	93.5	666	1	A36026	kinesin-related pr
686	4.2	93.5	668	2	T08725	probable finger pr

No.	Accession	n	Len	Score	%	Description
687	F86290	2	710	4.2	93.5	hypothetical prote
688	F90542	2	771	4.2	93.5	phosphoglycerate k
689	A32294	2	775	4.2	93.5	transposable eleme
690	T31433	2	1014	4.2	93.5	Na+/Ca2+-exchan
691	A34755	1	1036	4.2	93.5	nitrogen regulator
692	AG2187	2	1038	4.2	93.5	hypothetical prote
693	XPBEA9	1	1048	4.2	93.5	large structural p
694	D86731	2	1063	4.2	93.5	hypothetical diver
695	T38459	2	1794	4.2	93.5	hypothetical diver
696	T14280	2	1829	4.2	93.5	RW1 protein - mous
697	T38495	2	1969	4.2	93.5	hypothetical prote
698	T30074	2	2153	4.2	93.5	hypothetical prote
699	A34203	2	2717	4.2	93.5	DNA-binding protei
700	A41948	1	2783	4.2	93.5	alpha-fetoprotein
701	T20771	2	4549	4.2	93.5	hypothetical prote
702	T20774	2	4667	4.2	93.5	hypothetical prote
703	S53365	2	94	4.2	93	mucin 5AC (clone C
704	H96711	2	222	4.2	93	hypothetical prote
705	T21789	2	272	4.2	93	hypothetical prote
706	F85895	2	337	4.2	93	probable membrane
707	T27051	2	476	4.2	93	hypothetical prote
708	T35677	2	507	4.2	93	probable hydrolase
709	G75348	2	533	4.2	93	conserved hypothet
710	S22835	2	650	4.2	93	alpha-agglutinin -
711	T37949	2	741	4.2	93	hypothetical PSU1-
712	T25795	2	805	4.2	93	hypothetical prote
713	S51342	2	817	4.2	93	verprolin - yeast
714	B53689	2	862	4.2	93	homeotic protein C
715	S41984	2	863	4.2	93	SIP1 protein - yea
716	A47283	2	873	4.2	93	calphotin - fruit
717	S68983	2	910	4.2	93	auxilin - bovine
718	A42681	2	943	4.2	93	centromere protein
719	T00050	2	1006	4.2	93	hypothetical prote
720	G90546	2	1099	4.2	93	conserved hypothet
721	A45773	2	1476	4.2	93	kelch protein, lon
722	S20117	2	1478	4.2	93	protein kinase, lon
723	T33152	2	1706	4.2	93	zinc finger protei
724	T31337	2	1711	4.2	93	1,4-beta-glucanase
725	I38902	1	1721	4.2	93	retinoblastoma bin
726	B71426	2	1942	4.2	93	hypothetical prote
727	A46151	2	2314	4.2	92.5	protein-tyrosine-p
728	A56922	2	2578	4.2	92.5	transcription fact
729	T33152	2	2957	4.2	92.5	hypothetical prote
730	S47439	2	304	4.2	92.5	zinc-finger protei
731	B47236	2	331	4.2	92.5	zinc-finger protei
732	JQ2174	2	357	4.2	92.5	hypothetical 39.2K
733	A47236	2	477	4.2	92.5	zinc-finger protei
734	B39481	2	486	4.2	92.5	serum response fac
735	B89614	2	495	4.2	92.5	protein C43C3.3 [i
736	S47439	2	506	4.2	92.5	I2 protein - Trypa
737	A55929	2	537	4.2	92.5	fiber protein - ca
738	ERADDG	1	543	4.2	92.5	fertilization-inde
739	E84771	2	582	4.2	92.5	gliotactin precurs
740	S65180	2	599	4.2	92.5	transcription fact
741	JQ0607	2	639	4.2	92.5	hypothetical prote
742	T27642	2	756	4.2	92.5	protein kinase - f
743	T48815	2	758	4.2	92.5	neurexin III-alpha
744	A47282	2	865	4.2	92.5	hypothetical prote
745	FOFVHB	1	875	4.2	92.5	gag-myc polyprotei
746	A56920	2	956	4.2	92.5	gliotactin precurs
747	T13350	2	1037	4.2	92.5	transcription fact
748	T16275	2	1045	4.2	92.5	hypothetical prote
749	S58147	2	1087	4.2	92.5	protein kinase - f
750	B48218	2	1471	4.2	92.5	glucan 1,4-alpha-g
751	T16055	2	1592	4.2	92.5	hypothetical prote
752	T14160	2	1651	4.2	92.5	transmembrane rece
753	F86348	2	2123	4.2	92.5	hypothetical prote
754	T14328	2	2302	4.2	92.5	protein-tyrosine-p
755	S18253	2	3712	4.2	92.5	laminin alpha-1 ch
756	C89921	2	3890	4.2	92.5	hypothetical prote
757	T25562	2	339	4.2	92	hypothetical prote
758	T40167	2	344	4.2	92	hypothetical prote
759	A56346	2	481	4.2	92	transcription fact
760	S62474	2	489	4.2	92	probable transcrip
761	S62439	2	530	4.2	92	hypothetical serin
762	S66147	2	566	4.2	92	transcription fact
763	T42671	2	613	4.2	92	hypothetical prote
764	T18227	2	629	4.2	92	hypothetical prote
765	E86787	2	653	4.2	92	disease resistance
766	T17462	2	768	4.2	92	ubiquitin protein
767	T39585	2	786	4.2	92	GTPase regulator a
768	F59430	2	814	4.2	92	hypothetical diver
769	AF2089	2	833	4.2	92	hypothetical prote
770	T17291	2	845	4.2	92	hypothetical prote
771	T49492	2	898	4.2	92	hypothetical prote
772	T16094	2	972	4.2	92	hypothetical prote
773	T13039	2	1019	4.2	92	tyrosine kinase re
774	A96719	2	1028	4.2	92	hypothetical prote
775	T43164	2	1080	4.2	92	lactA protein - Li
776	B41206	2	1125	4.2	92	microtubule-associ
777	T39174	2	1283	4.2	92	hypothetical Serin
778	S42718	2	1475	4.2	92	nuclear pore compl
779	T17120	2	1742	4.2	92	cellulase (EC 3.2.
780	A54970	2	1744	4.2	92	tensin, cardiac mu
781	A56577	2	2364	4.2	92	microtubule-associ
782	QRMSP1	2	2464	4.2	92	microtubule-associ
783	F84522	2	191	4.1	91.5	probable proline-r
784	T10737	2	214	4.1	91.5	extensin-like cell
785	B86433	2	319	4.1	91.5	RAD 23B protein -
786	JC7783	2	385	4.1	91.5	hypothetical prote
787	S67439	2	390	4.1	91.5	hypothetical prote
788	I38488	2	426	4.1	91.5	trophinin - human
789	A32575	2	489	4.1	91.5	C-ski protein FB29
790	B33416	2	490	4.1	91.5	lymphocyte homing
791	I48162	2	587	4.1	91.5	nuclear factor I -
792	JC7776	2	616	4.1	91.5	cytochrome P450 -
793	T41681	2	650	4.1	91.5	extracellular prot
794	S16706	2	650	4.1	91.5	matrix metalloprot
795	S33316	2	681	4.1	91.5	probable serine/th
796	I38488	2	749	4.1	91.5	transcription acti
797	A32575	2	750	4.1	91.5	structural protein
798	T23129	2	808	4.1	91.5	hypothetical prote
799	T25144	2	813	4.1	91.5	hypothetical prote
800	A56823	2	902	4.1	91.5	DNA-directed RNA p
801	AD1374	2	940	4.1	91.5	internalin protein
802	A96748	2	946	4.1	91.5	hypothetical prote
803	S66736	2	1081	4.1	91.5	transcription acti
804	T23472	2	1221	4.1	91.5	hypothetical prote
805	T15316	2	1223	4.1	91.5	hypothetical prote
806	A48954	2	1331	4.1	91.5	mannan endo-1,4-be
807	T24212	2	1422	4.1	91.5	hypothetical prote
808	H64106	2	1694	4.1	91.5	IgA-specific metal
809	T00391	2	1736	4.1	91.5	hypothetical prote
810	A43359	2	2774	4.1	91.5	microtubule-associ
811	T03099	2	13288	4.1	91.5	mucin, submaxillar
812	B37994	2	282	4.1	91	mucin, submaxillar
813	D44355	2	301	4.1	91	RF2 protein - saim
814	D82572	2	400	4.1	91	CD44 glycoprotein
815	A24993	2	449	4.1	91	TonB protein XF232
816	AG1506	2	465	4.1	91	cellulase (EC 3.2.
817	AF1700	2	491	4.1	91	P60 extracellular
818	WJFFEN	2	552	4.1	91	UDP-N-acetylmuramo
819	F84718	2	571	4.1	91	homeotic protein e
820	ERADF5	1	581	4.1	91	hypothetical prote
821	B75556	2	597	4.1	91	fiber protein - hu
822	T38656	2	609	4.1	91	hypothetical prote
823	S70520	2	613	4.1	91	probable RNA-bindi
824	S41314	2	630	4.1	91	melatonin receptor
825	S59630	2	650	4.1	91	hypothetical prote
826	E84682	2	653	4.1	91	dystroglycan alpha
827	S63587	2	667	4.1	91	hypothetical prote
828	S20902	2	681	4.1	91	gene pacC protein
829	A48128	2	733	4.1	91	mating type protei
830	T16726	2	760	4.1	91	P3A2 DNA binding p
831	A55448	2	776	4.1	91	hypothetical prote
832	T22182	2	843	4.1	91	Ah receptor nuclea

No.	Accession	n	Length	Score	%	Description
833	S50670	2	851	4.1	91	BCK2 protein - yea
834	D89756	2	880	4.1	91	protein T23E7.2b [
835	T23807	2	882	4.1	91	hypothetical prote
836	S20582	2	895	4.1	91	dystrophin-associa
837	S36326	2	896	4.1	91	clathrin assembly
838	S36327	2	915	4.1	91	protein F39D8.1b [
839	D89723	2	940	4.1	91	hypothetical prote
840	T21998	2	945	4.1	91	ice nucleation pro
841	T03511	2	951	4.1	91	mineralocorticoid
842	A41401	2	981	4.1	91	surface layer prot
843	T00046	2	1004	4.1	91	probable tail fibe
844	G64887	2	1122	4.1	91	probable transcrip
845	T13283	2	1221	4.1	91	major capsid prote
846	T41960	2	1345	4.1	91	versican precursor
847	T14274	2	1643	4.1	91	hypothetical prote
848	T34249	2	1817	4.1	91	probable membrane
849	S48405	2	2376	4.1	91	versican precursor
850	A60979	2	2409	4.1	91	notch protein homo
851	S18188	2	2531	4.1	91	probable invasin Z
852	E85822	2	2660	4.1	91	versican precursor
853	T42389	2	3381	4.1	91	ankyrin 2, neurona
854	S37431	2	3924	4.1	91	FK506 polyketide s
855	T17428	2	7576	4.1	91	probable membrane
856	S67295	2	204	4.1	90.5	promastigote surfa
857	B41710	2	243	4.1	90.5	vanadate resistanc
858	S65174	2	260	4.1	90.5	hypothetical prote
859	S46760	2	325	4.1	90.5	hypothetical prote
860	T15727	2	336	4.1	90.5	peptidyl-prolyl ci
861	E75341	2	350	4.1	90.5	protein F58A4.7b [
862	B85561	2	382	4.1	90.5	hypothetical prote
863	T33663	2	424	4.1	90.5	endo-1,4-beta-xyla
864	JC5861	2	429	4.1	90.5	hypothetical prote
865	T31483	2	456	4.1	90.5	probable membrane
866	T36256	2	464	4.1	90.5	hypothetical prote
867	T43488	2	505	4.1	90.5	hypothetical prote
868	T25807	2	532	4.1	90.5	autolysin, N-acety
869	AH1786	2	594	4.1	90.5	probable transcrip
870	T16677	2	601	4.1	90.5	hypothetical prote
871	T21428	1	643	4.1	90.5	finger protein MSN
872	S39004	2	704	4.1	90.5	G-box-binding fact
873	A53185	1	708	4.1	90.5	transcription fact
874	A34873	1	739	4.1	90.5	metal-regulatory t
875	S48059	2	753	4.1	90.5	transducin-like en
876	B56695	2	770	4.1	90.5	internalin A precu
877	S37387	2	800	4.1	90.5	gag-myc polyprotei
878	FOFV29	1	875	4.1	90.5	phosphoprotein, sy
879	A44825	2	901	4.1	90.5	transcription fact
880	A48085	2	927	4.1	90.5	hypothetical prote
881	E96683	2	1006	4.1	90.5	hypothetical prote
882	T19734	2	1043	4.1	90.5	hypothetical prote
883	B86748	2	1093	4.1	90.5	DNA-binding protei
884	B75625	2	1145	4.1	90.5	neurocan precursor
885	S26650	2	1203	4.1	90.5	latrophilin-2 (spl
886	S28764	2	1257	4.1	90.5	latrophilin-2 (spl
887	T18381	2	1407	4.1	90.5	latrophilin-2, (spl
888	T18385	2	1420	4.1	90.5	latrophilin-2, (spl
889	T18383	2	1422	4.1	90.5	latrophilin-2 (spl
890	T18387	2	1435	4.1	90.5	latrophilin-2 (spl
891	T18382	2	1450	4.1	90.5	latrophilin-2 (spl
892	T18386	2	1463	4.1	90.5	latrophilin-2 (spl
893	T18384	2	1465	4.1	90.5	extracellular matr
894	T18388	2	1478	4.1	90.5	probable polyketid
895	T31110	2	2055	4.1	90.5	adenomatous polypo
896	T03223	2	2100	4.1	90.5	hypothetical prote
897	T30258	2	2274	4.1	90.5	probable iron tran
898	T37629	2	277	4.1	90	probable modD prot
899	AF0489	2	319	4.1	90	subtilisin (EC 3.4
900	D70666	2	325	4.1	90	mating pheromone r
901	SUBSI	1	381	4.1	90	pre-mrna splicing
902	T50335	2	404	4.1	90	activating transcr
903	T38149	2	481	4.1	90	transcription fact
904	JC4028	2	486	4.1	90	
905	S01038	2	499	4.1	90	

No.	Accession	n	Length	Score	%	Description
906	S45571	2	510	4.1	90	nuclear factor I-C
907	AF2351	2	564	4.1	90	serine/threonine k
908	T06292	2	600	4.1	90	hypothetical prote
909	T39866	2	603	4.1	90	hypothetical prote
910	T19206	2	646	4.1	90	neuregulin-3 [impo
911	T44447	2	713	4.1	90	CT456 hypothetical
912	H86561	2	755	4.1	90	hypothetical prote
913	B72061	2	776	4.1	90	hypothetical prote
914	T33543	2	778	4.1	90	erythrocyte-bindin
915	A35970	2	781	4.1	90	XynB precursor - R
916	S51592	2	810	4.1	90	hypoxia-inducible
917	JC4837	2	884	4.1	90	unknown protein, 4
918	E86244	2	912	4.1	90	ubiquitin-specific
919	B44450	2	980	4.1	90	probable cell divi
920	G75523	2	1019	4.1	90	probable disease r
921	C96519	2	1070	4.1	90	hypothetical prote
922	T34385	2	1092	4.1	90	protein T22C5.3 [i
923	B86401	2	1106	4.1	90	hypothetical prote
924	T31742	2	1219	4.1	90	nucleoporin Nup153
925	T14578	2	1237	4.1	90	probable outer mem
926	D71850	2	1262	4.1	90	protein stn-B - fr
927	T13353	2	1387	4.1	90	G-protein signalin
928	JC5502	2	1468	4.1	90	hypothetical prote
929	T05672	2	1602	4.1	90	Rab3 GDP/GTP excha
930	T31671	2	1732	4.1	90	integrin beta-4 ch
931	B71442	2	1875	4.1	90	hypothetical prote
932	A36429	2	1974	4.1	90	probable starch sy
933	T16703	2	238	4.1	90	probable membrane
934	T07921	2	389	4.0	89.5	probable transcrip
935	S53975	2	391	4.0	89.5	hypothetical prote
936	S61704	2	415	4.0	89.5	hypothetical prote
937	T19099	2	420	4.0	89.5	methyl-accepting c
938	T45592	2	433	4.0	89.5	probable peptidogl
939	D82077	2	439	4.0	89.5	oligodendrocyte-my
940	AB1251	2	440	4.0	89.5	myocyte-specific e
941	A39613	2	507	4.0	89.5	response regulator
942	S25831	2	522	4.0	89.5	chitinase (EC 3.2.
943	T43417	2	535	4.0	89.5	hypothetical prote
944	S65762	2	586	4.0	89.5	conserved hypothet
945	T29695	2	587	4.0	89.5	hypothetical prote
946	AG3019	2	608	4.0	89.5	internalin like pr
947	T37864	2	620	4.0	89.5	hypothetical prote
948	AG1598	2	634	4.0	89.5	somatotropin recep
949	B98265	2	638	4.0	89.5	glucan 1,4-alpha-g
950	S12136	2	639	4.0	89.5	membrane glycoprot
951	JT0479	2	651	4.0	89.5	internalin protein
952	C56653	2	673	4.0	89.5	probable membrane
953	AF1143	2	675	4.0	89.5	F28L22.6 protein -
954	S59379	2	719	4.0	89.5	chitinase B homolo
955	B86490	2	756	4.0	89.5	pyocin S3 - Pseudo
956	AB1088	2	766	4.0	89.5	hypothetical prote
957	A56394	2	799	4.0	89.5	hypothetical prote
958	S75351	2	800	4.0	89.5	Internalin A [impo
959	AB1129	2	883	4.0	89.5	puff 74E protein -
960	S04722	2	894	4.0	89.5	hypothetical prote
961	T49299	2	1102	4.0	89.5	hypothetical prote
962	T39943	2	1216	4.0	89.5	protein F40H6.5 [i
963	F88473	2	1276	4.0	89.5	probable membrane
964	S69048	2	1358	4.0	89.5	hypothetical prote
965	T22699	2	1360	4.0	89.5	hypothetical prote
966	T33922	2	1447	4.0	89.5	tumor suppressor p
967	A54100	2	1507	4.0	89.5	natural killer cel
968	B47328	2	1902	4.0	89.5	lactocepin (EC 3.4
969	B45764	2	2441	4.0	89.5	CREB-binding prote
970	S39161	2	4861	4.0	89.5	giant protein p619
971	S71752	2	265	4.0	89.5	hypothetical prote
972	T33695	2	281	4.0	89	hypothetical prote
973	D84307	2	379	4.0	89	conserved hypothet
974	AE3003	2	381	4.0	89	subtilisin (EC 3.4
975	JH0778	2	432	4.0	89	hypothetical prote
976	T08771	2	452	4.0	89	hypothetical 28.0K
977	D98280	2	458	4.0	89	hypothetical prote
978	B87335	2		4.0	89	hypothetical prote

No	%	Score	Len	Accession	N	Description
979	89	4.0	485	S36184	2	translation elonga
980	89	4.0	506	AG1864	2	hypothetical prote
981	89	4.0	524	S33640	2	homeotic protein s
982	89	4.0	545	A48448	2	early expression g
983	89	4.0	635	T15904	2	hypothetical prote
984	89	4.0	639	T23424	2	hypothetical prote
985	89	4.0	668	B86831	2	hypothetical prote
986	89	4.0	768	A42755	2	P-selectin precurs
987	89	4.0	884	T20405	2	hypothetical prote
988	89	4.0	892	T09071	2	SH3 domains-contai
989	89	4.0	947	T01238	2	hypothetical prote
990	89	4.0	989	D89852	2	fibrinogen-binding
991	89	4.0	1026	A48995	2	paracrystalline su
992	89	4.0	1027	I38759	2	zinc finger/leucin
993	89	4.0	1051	JC4091	2	glycoprotein A - P
994	89	4.0	1073	C87374	2	S-layer protein Rs
995	89	4.0	1120	T01863	2	hypothetical prote
996	89	4.0	1135	I61186	2	alpha-7 integrin -
997	89	4.0	1209	T00373	2	hypothetical prote
998	89	4.0	1244	S25327	2	cytoskeleton assem
999	89	4.0	1365	S14871	2	suppressor two of
1000	89	4.0	1719	T30174	2	exoribonuclease, v
1001	89	4.0	1723	H86557	2	polymorphic membra
1002	89	4.0	1723	E72067	2	polymorphic membra
1003	89	4.0	1732	C81601	2	polymorphic membra
1004	89	4.0	1748	JQ1555	2	genome polyprotein
1005	89	4.0	1772	A45532	2	major merozoite su
1006	89	4.0	1830	A37981	2	microtubule-associ
1007	89	4.0	2422	T12687	2	ALR protein homolo
1008	89	4.0	2508	S61441	2	surface-associated
1009	89	4.0	2531	A46019	2	notch-1 protein -
1010	89	4.0	3122	T17202	2	DNA-directed DNA p
1011	89	4.0	3375	T19821	2	hypothetical prote
1012	88.5	4.0	153	S67294	2	hypothetical prote
1013	88.5	4.0	182	T30078	2	hypothetical membra
1014	88.5	4.0	254	D88560	2	protein F58A4.1 [li
1015	88.5	4.0	286	A70168	2	hypothetical prote
1016	88.5	4.0	322	A44278	1	structural protein
1017	88.5	4.0	330	S47492	2	genome polyprotein
1018	88.5	4.0	330	S30577	2	genome polyprotein
1019	88.5	4.0	413	H87604	2	hypothetical prote
1020	88.5	4.0	414	AD1027	2	probable exported
1021	88.5	4.0	415	S35760	2	fcrA protein precu
1022	88.5	4.0	416	T23977	2	hypothetical prote
1023	88.5	4.0	439	T18898	2	hypothetical prote
1024	88.5	4.0	458	T33308	2	hypothetical prote
1025	88.5	4.0	461	JN0097	2	secreted 45K prote
1026	88.5	4.0	487	AE0488	2	probable membrane
1027	88.5	4.0	503	G75262	2	hypothetical prote
1028	88.5	4.0	530	G32812	2	hypothetical prote
1029	88.5	4.0	557	S34412	1	transcription fact
1030	88.5	4.0	593	JC7829	2	metal-responsive t
1031	88.5	4.0	596	S58106	2	hypothetical 65.9
1032	88.5	4.0	644	T16136	2	hypothetical prote
1033	88.5	4.0	661	T16597	2	hypothetical prote
1034	88.5	4.0	676	T32556	2	hypothetical prote
1035	88.5	4.0	744	T39841	2	topisomerase II as
1036	88.5	4.0	796	AG0523	2	glucose dehydrogen
1037	88.5	4.0	801	T29018	2	hypothetical prote
1038	88.5	4.0	805	JC7635	2	aryl hydrocarbon r
1039	88.5	4.0	811	S04085	2	ovarian tumor prot
1040	88.5	4.0	860	A96717	2	unknown protein, 4
1041	88.5	4.0	971	B90835	2	probable tail fibe
1042	88.5	4.0	973	C85693	2	probable membrane
1043	88.5	4.0	1018	A32192	2	fibronectin-bindin
1044	88.5	4.0	1131	T15787	2	hypothetical prote
1045	88.5	4.0	1165	S62982	2	vacuolar protein V
1046	88.5	4.0	1202	S55553	2	LAR-interacting pr
1047	88.5	4.0	1221	A49457	2	fibulin-2 precurso
1048	88.5	4.0	1257	T09493	2	period protein hom
1049	88.5	4.0	1319	C43735	1	bcsC protein - Ace
1050	88.5	4.0	1325	T25753	2	hypothetical prote
1051	88.5	4.0	1337	T30291	2	dextranase - Strep
1052	88.5	4.0	1505	JC4851	2	hypoxia-inducibl
1053	88.5	4.0	1630	T00390	2	KIAA0614 protein -
1054	88.5	4.0	1677	T46095	2	hypothetical prote
1055	88.5	4.0	1902	S06997	2	lactocepin (EC 3.4
1056	88.5	4.0	3534	T42567	2	tegument protein 2
1057	88	4.0	98	S53504	2	mucin 5AC (clone M
1058	88	4.0	228	A41776	2	extensin-like prot
1059	88	4.0	310	A42656	2	syndecan 1 precurs
1060	88	4.0	324	T50128	2	hypothetical serin
1061	88	4.0	326	A48952	2	hypothetical serin
1062	88	4.0	358	JT0579	2	triacylglycerol li
1063	88	4.0	364	I48188	2	triacylglycerol li
1064	88	4.0	364	T25280	2	gene NKx6.1 protei
1065	88	4.0	382	RRNZVT	1	polymerase-associa
1066	88	4.0	395	A60058	2	neural cell adhesi
1067	88	4.0	421	T15416	2	hypothetical prote
1068	88	4.0	463	T39983	2	serine proline ric
1069	88	4.0	501	T21440	2	hypothetical prote
1070	88	4.0	521	S25478	1	heat shock transcr
1071	88	4.0	527	S61154	2	hypothetical prote
1072	88	4.0	557	T15551	2	hypothetical prote
1073	88	4.0	673	D89447	2	hypothetical prote
1074	88	4.0	770	JH0797	2	protein F57C12.1 [
1075	88	4.0	799	I52835	2	castor protein - f
1076	88	4.0	824	T20422	2	H-NUC - human
1077	88	4.0	849	T21621	2	hypothetical prote
1078	88	4.0	878	T39081	2	hypothetical prote
1079	88	4.0	886	T19361	2	hypothetical prote
1080	88	4.0	925	S39344	2	hypothetical prote
1081	88	4.0	926	B72537	2	deubiquinating enz
1082	88	4.0	930	T08599	2	hypothetical prote
1083	88	4.0	1098	T20140	2	probable transcrip
1084	88	4.0	1113	F69823	2	hypothetical prote
1085	88	4.0	1217	E64664	2	probable phosphoes
1086	88	4.0	1230	S49645	2	outer membrane pro
1087	88	4.0	1251	T30565	2	probable membrane
1088	88	4.0	1338	A57655	2	MAP kinase kinase
1089	88	4.0	1388	T17411	2	tim (timeless) pro
1090	88	4.0	1562	T18272	2	probable polyketide synthas
1091	88	4.0	1570	C81675	2	1-phosphatidylinos
1092	88	4.0	1672	D64962	2	polymorphic membra
1093	88	4.0	2383	A56923	2	probable membrane
1094	88	4.0	2529	S11661	2	transcription fact
1095	88	4.0	2541	T24157	2	talin - mouse
1096	88	4.0	2606	E88320	2	hypothetical prote
1097	88	4.0	2738	A55575	2	protein F07A1.6 [
1098	88	4.0	4377	A87483	2	ankyrin 3, long sp
1099	87.5	4.0	223	T29210	2	hypothetical prote
1100	87.5	4.0	226	T38618	2	hypothetical prote
1101	87.5	4.0	229	S64423	2	probable spliceosom
1102	87.5	4.0	259	T37391	2	probable membrane
1103	87.5	4.0	272	T51437	2	membrane associate
1104	87.5	4.0	275	C39112	2	hypothetical prote
1105	87.5	4.0	280	T43463	2	merozoite 45K surf
1106	87.5	4.0	295	B69956	2	hypothetical prote
1107	87.5	4.0	309	T39110	2	phosphate ABC tran
1108	87.5	4.0	320	T18853	2	probable gtpase ac
1109	87.5	4.0	399	A12462	2	probable transcrip
1110	87.5	4.0	401	E88736	2	hypothetical prote
1111	87.5	4.0	412	A57468	2	protein F33D4.6a [
1112	87.5	4.0	412	S53916	2	P-selectin glycopr
1113	87.5	4.0	420	T48724	2	SUN4 protein precu
1114	87.5	4.0	425	A36372	2	hypothetical prote
1115	87.5	4.0	437	S52751	2	membrane transport
1116	87.5	4.0	448	E86903	2	heat shock transcr
1117	87.5	4.0	456	E96740	2	hypothetical prote
1118	87.5	4.0	461	T51044	2	hypothetical prote
1119	87.5	4.0	461	T42679	2	related to spore c
1120	87.5	4.0	462	JC8060	2	hypothetical prote
1121	87.5	4.0	493	T41015	2	smoothelin-like ac
1122	87.5	4.0	497	B44443	2	proline rich prote
1123	87.5	4.0	535		2	hypothetical prote
1124	87.5	4.0	550	T29919	2	hypothetical prote

No.	Description	Accession	N	Length	Score	%
1125	probable fadD30 pr	C70634	2	585	4.0	87.5
1126	hypothetical C2H2	T39291	2	637	4.0	87.5
1127	hypothetical prote	H82690	2	638	4.0	87.5
1128	notch2 protein hom	S03547	2	639	4.0	87.5
1129	hypothetical prote	A56695	2	664	4.0	87.5
1130	hypothetical prote	T32557	2	672	4.0	87.5
1131	hypothetical prote	T00369	2	677	4.0	87.5
1132	UDP-sugar hydrolas	C84295	2	682	4.0	87.5
1133	hypothetical prote	T25519	2	691	4.0	87.5
1134	epican - human	I37369	2	699	4.0	87.5
1135	gag polyprotein -	S11454	2	701	4.0	87.5
1136	dendritic cell-der	JC7679	2	733	4.0	87.5
1137	hypothetical prote	T34329	2	747	4.0	87.5
1138	hypothetical prote	T00366	2	780	4.0	87.5
1139	probable membrane	T02812	2	823	4.0	87.5
1140	discs-large tumor	A39651	1	960	4.0	87.5
1141	carboxymethylcellu	S03818	2	962	4.0	87.5
1142	ice nucleation pro	AE3045	2	989	4.0	87.5
1143	hypothetical prote	G98240	2	1009	4.0	87.5
1144	HPI layer surface	A29832	2	1036	4.0	87.5
1145	A-kinase anchoring	T42732	2	1129	4.0	87.5
1146	stripe a/b protein	S69205	2	1180	4.0	87.5
1147	AF-4 protein, spli	I39410	2	1210	4.0	87.5
1148	serine/proline-ric	A58198	2	1213	4.0	87.5
1149	protein F27F5.19 [	F96509	2	1309	4.0	87.5
1150	hypothetical prote	T39066	2	1318	4.0	87.5
1151	hypothetical prote	T40839	2	1364	4.0	87.5
1152	KIAA1204 protein [	A59437	2	1445	4.0	87.5
1153	hypothetical prote	T00273	2	1520	4.0	87.5
1154	supervillin P205 -	T08878	2	1792	4.0	87.5
1155	probable GTPase-ac	T14106	2	1822	4.0	87.5
1156	microtubule-associ	QRHUMT	1	1824	4.0	87.5
1157	immunoglobulin A1	C95008	2	1856	4.0	87.5
1158	genome polyprotein	JQ0533	1	1874	4.0	87.5
1159	hypothetical prote	T33216	2	1965	4.0	87.5
1160	hypothetical prote	S77257	2	1978	4.0	87.5
1161	hypothetical prote	AC2403	2	182	3.9	87
1162	mucin JUL10 - huma	T11592	2	319	3.9	87
1163	DNA-binding protei	S37595	2	330	3.9	87
1164	hemagglutinin HA1	A37991	2	342	3.9	87
1165	hypothetical prote	HMIVTA	1	343	3.9	87
1166	hypothetical prote	T48827	2	344	3.9	87
1167	hypothetical prote	T46916	2	346	3.9	87
1168	tenascin - rat (fr	T38443	2	383	3.9	87
1169	hypothetical prote	T38442	2	383	3.9	87
1170	transcription fact	S35719	1	399	3.9	87
1171	CD44 protein - mou	S30397	2	414	3.9	87
1172	hypothetical serin	T50279	2	416	3.9	87
1173	chemotaxis MotB pr	AC0203	2	427	3.9	87
1174	elkl protein - mou	JC4965	2	429	3.9	87
1175	probable F25E5.4 [i	A89102	2	481	3.9	87
1176	probable variable	AB0929	2	504	3.9	87
1177	61K protein - Auto	S25128	2	543	3.9	87
1178	thiol,disulfide in	AI0042	2	595	3.9	87
1179	hypothetical prote	B84520	2	629	3.9	87
1180	probable cell surf	AD1525	2	657	3.9	87
1181	hypothetical prote	T29708	2	718	3.9	87
1182	probable membrane	S56277	2	733	3.9	87
1183	hypothetical prote	T31732	2	779	3.9	87
1184	PAM1 protein - yea	S54547	2	830	3.9	87
1185	aryl hydrocarbon r	JC7993	2	834	3.9	87
1186	eyeless, long form	I45557	2	838	3.9	87
1187	hypothetical prote	F96531	2	847	3.9	87
1188	major nitrogen reg	S51493	2	862	3.9	87
1189	probable gamma-ada	T41685	2	865	3.9	87
1190	A-alpha Z 4 protei	D37271	2	930	3.9	87
1191	probable serine/th	S28394	2	939	3.9	87
1192	embryo kinase 5 -	A56599	2	995	3.9	87
1193	probable membrane	S45801	2	1057	3.9	87
1194	transcription fact	A57410	2	1065	3.9	87
1195	verprolin related	T50949	2	1072	3.9	87
1196	neural cell adhesi	IJMSNL	1	1115	3.9	87
1197	delta-crystallin/E	JC4934	2	1117	3.9	87
1198	extensin-like prot	S49915	2	1188	3.9	87
1199	ROM2 protein - yea	S51389	2	1356	3.9	87
1200	Cl1AA protein - ra	T17138	2	1466	3.9	87
1201	latrophilin-1, bra	T18411	2	1467	3.9	87
1202	Cl1BA protein - ra	T17149	2	1471	3.9	87
1203	latrophilin-1, bra	T18413	2	1472	3.9	87
1204	Cl1AB protein - ra	T17145	2	1510	3.9	87
1205	Cl1BB protein - ra	T17156	2	1515	3.9	87
1206	hypothetical prote	T00344	2	1533	3.9	87
1207	hypothetical prote	S67083	2	1619	3.9	87
1208	microtubule-associ	S13507	2	1825	3.9	87
1209	hypothetical prote	T15962	2	1879	3.9	87
1210	KIAA1424 protein [	A59438	2	1944	3.9	87
1211	fxbC protein - Myc	T14182	2	2129	3.9	87
1212	zonadhesin - pig	T34022	2	2476	3.9	87
1213	peptide synthetase	T14164	2	2569	3.9	87
1214	hypothetical prote	T29285	2	2761	3.9	87
1215	adenomatous polypo	RBHUAP	1	2843	3.9	87
1216	All-1 protein +GTE	A48205	2	3869	3.9	87
1217	hypothetical prote	S76412	2	4199	3.9	87
1218	cyclosporin synthe	S41309	2	15281	3.9	87
1219	cold shock protein	S61310	2	251	3.9	86.5
1220	hypothetical prote	S60947	2	265	3.9	86.5
1221	probable DNA-bindi	AC0822	2	324	3.9	86.5
1222	hypothetical prote	T15837	2	336	3.9	86.5
1223	hypothetical prote	T34510	2	360	3.9	86.5
1224	conserved hypothet	H98105	2	380	3.9	86.5
1225	polymerase-associa	RRNZP2	1	395	3.9	86.5
1226	exported serine pr	H86891	2	408	3.9	86.5
1227	hypothetical prote	T32467	2	415	3.9	86.5
1228	probable valine-py	E75378	2	420	3.9	86.5
1229	glycoprotein gp63	VGBEE9	1	424	3.9	86.5
1230	hypothetical prote	T17289	2	433	3.9	86.5
1231	probable lipoprote	T34992	2	447	3.9	86.5
1232	flagellar hook-ass	AF0224	2	466	3.9	86.5
1233	merozoite surface	B44997	2	476	3.9	86.5
1234	hypothetical prote	S09880	2	499	3.9	86.5
1235	hypothetical prote	T34178	2	525	3.9	86.5
1236	hypothetical prote	A56596	2	554	3.9	86.5
1237	hypothetical prote	S39297	2	556	3.9	86.5
1238	chitinase (EC 3.2.	S15342	2	557	3.9	86.5
1239	fiber protein - hu	T20709	2	559	3.9	86.5
1240	transcription fact	AG2008	2	567	3.9	86.5
1241	hypothetical prote	A54861	2	575	3.9	86.5
1242	hypothetical prote	D70863	2	592	3.9	86.5
1243	hypothetical prote	T34392	2	615	3.9	86.5
1244	protein kinase 1 (	JC6534	1	627	3.9	86.5
1245	probable transcrip	T38023	2	630	3.9	86.5
1246	transcription fact	S35574	2	634	3.9	86.5
1247	somatotropin recep	A33505	2	638	3.9	86.5
1248	type I transmembra	A45705	2	681	3.9	86.5
1249	gag polyprotein -	F48613	2	701	3.9	86.5
1250	gag polyprotein -	D48613	2	701	3.9	86.5
1251	phenylalanine ammo	S01999	2	713	3.9	86.5
1252	probable phosphoes	P72693	2	728	3.9	86.5
1253	folded gastrulatio	A53064	2	730	3.9	86.5
1254	lymphocyte homing	A47195	2	742	3.9	86.5
1255	probable FCA gamma	E71429	1	747	3.9	86.5
1256	hypothetical prote	AB2225	2	760	3.9	86.5
1257	protein H05C05.1 [	C88402	2	828	3.9	86.5
1258	ecdysone-induced p	A34692	2	829	3.9	86.5
1259	hypothetical prote	T30479	2	884	3.9	86.5
1260	protein kinase 1 -	A38903	2	891	3.9	86.5
1261	hypothetical prote	B84483	2	928	3.9	86.5
1262	LcKin kinesin-rela	A47334	2	955	3.9	86.5
1263	hypothetical prote	T00353	2	968	3.9	86.5
1264	protein-tyrosine k	I50611	2	988	3.9	86.5
1265	hypothetical prote	T29776	2	1046	3.9	86.5
1266	period clock prote	S02035	2	1087	3.9	86.5
1267	probable serine/th	T18611	2	1192	3.9	86.5
1268	protein H39E23.1 [	G89287	2	1246	3.9	86.5
1269	cortactin-binding	T14272	2	1252	3.9	86.5
1270	hypothetical prote	B86807	2	1441	3.9	86.5

#	%ID	Val	Num	Ct	Accession	Description
1271	86.5	3.9	1469	2	T19168	hypothetical prote
1272	86.5	3.9	1518	2	PQ0221	polyprotein - plum
1273	86.5	3.9	1603	2	A48613	gag/pol polyprotei
1274	86.5	3.9	2145	2	JC4747	adenylate cyclase
1275	86.5	3.9	2195	1	S61103	SEC16 protein - ye
1276	86.5	3.9	2351	1	EZHU	coagulation factor
1277	86.5	3.9	2469	2	H36812	hypothetical prote
1278	86.5	3.9	3282	2	E82750	hemagglutinin-like
1279	86.5	3.9	3442	2	E82589	hemagglutinin-like
1280	86.5	3.9	3455	2	B82519	hemagglutinin-like
1281	86	3.9	116	2	E48338	hypothetical prote
1282	86	3.9	229	2	AG2171	hypothetical prote
1283	86	3.9	230	2	I46918	leucine-rich glyco
1284	86	3.9	288	2	PH1917	FL-160-1 protein -
1285	86	3.9	302	2	T10033	hypothetical prote
1286	86	3.9	334	2	C96987	glyceraldehyde 3-p
1287	86	3.9	349	2	T05857	hypothetical prote
1288	86	3.9	349	2	T16882	hypothetical prote
1289	86	3.9	354	2	A35788	hemagglutinin - in
1290	86	3.9	358	2	AD2378	hypothetical prote
1291	86	3.9	366	2	T24546	hypothetical prote
1292	86	3.9	381	1	SUBSS	subtilisin (EC 3.4
1293	86	3.9	381	2	JQ1487	subtilisin (EC 3.4
1294	86	3.9	391	2	PD0035	sterol regulatory
1295	86	3.9	394	1	VGBE17	glycoprotein D pre
1296	86	3.9	394	1	VGBED1	glycoprotein D - h
1297	86	3.9	396	2	T35659	probable transmemb
1298	86	3.9	432	2	JS0306	microtubule-associ
1299	86	3.9	433	2	T49675	origin recognition
1300	86	3.9	467	2	JC7923	microtubule-associ
1301	86	3.9	503	2	A54868	nuclear respirator
1302	86	3.9	512	2	F75638	probable oxidative
1303	86	3.9	527	1	S25481	heat shock transcr
1304	86	3.9	535	2	A53671	protein-tyrosine-p
1305	86	3.9	569	2	A46462	T cell activation
1306	86	3.9	640	1	S76024	conserved hypothet
1307	86	3.9	656	2	S65826	hypothetical prote
1308	86	3.9	681	2	AC1458	surface anchored p
1309	86	3.9	684	2	T01267	leucine-rich repea
1310	86	3.9	699	2	A96529	hypothetical prote
1311	86	3.9	710	2	S30154	low-temperature-in
1312	86	3.9	732	2	T25937	hypothetical prote
1313	86	3.9	772	2	A55004	transcription fact
1314	86	3.9	796	1	JC1285	protein-tyrosine-p
1315	86	3.9	804	2	S64090	SCY1 protein - yea
1316	86	3.9	816	2	S64439	hypothetical prote
1317	86	3.9	836	2	T21631	hypothetical prote
1318	86	3.9	841	2	JC5894	killer cell inhibi
1319	86	3.9	915	2	S54485	CES1 protein - yea
1320	86	3.9	932	2	S09151	suvar(3)7 protein
1321	86	3.9	1116	2	S77213	DNA-directed DNA p
1322	86	3.9	1132	2	B82538	ribonuclease E XF2
1323	86	3.9	1173	2	I50620	prockr2 - chicken
1324	86	3.9	1209	2	T14357	homeodomain-intera
1325	86	3.9	1211	2	T08540	hypothetical prote
1326	86	3.9	1276	2	T02711	transcription fact
1327	86	3.9	1291	2	A28334	protein-tyrosine-p
1328	86	3.9	1300	1	T18364	ro-3 protein - Neu
1329	86	3.9	1309	2	H96650	protein T3P18.3 [i
1330	86	3.9	1396	2	A44453	translation initia
1331	86	3.9	1429	2	T41699	killer cell inhibi
1332	86	3.9	1541	2	A37023	C2-domain family p
1333	86	3.9	1545	2	B41859	IgA-specific metal
1334	86	3.9	1560	2	T02885	peroxisome prolife
1335	86	3.9	1606	2	T49219	translation initia
1336	86	3.9	1731	2	AB3045	ice nucleation pro
1337	86	3.9	1731	2	B98241	hypothetical prote
1338	86	3.9	1751	2	G71518	hypothetical prote
1339	86	3.9	2023	1	T13154	polycomb protein e
1340	86	3.9	2132	2	A55182	aggrecan precursor
1341	86	3.9	2468	2	A83412	hypothetical prote
1342	85.5	3.9	208	2	A87269	hypothetical prote
1343	85.5	3.9	222	2	T16381	hypothetical prote

#	%ID	Val	Num	Ct	Accession	Description
1344	85.5	3.9	374	2	T33844	hypothetical prote
1345	85.5	3.9	382	2	A48492	polysaccharide exp
1346	85.5	3.9	406	2	A35360	otefin - fruit fly
1347	85.5	3.9	424	2	T32434	hypothetical prote
1348	85.5	3.9	425	2	A38153	paired box protein
1349	85.5	3.9	447	2	S42805	gag-like polyprote
1350	85.5	3.9	453	2	C40511	hypothetical prote
1351	85.5	3.9	465	2	S03325	transforming prote
1352	85.5	3.9	491	2	B75554	hypothetical prote
1353	85.5	3.9	493	2	S13530	CD44E protein, epi
1354	85.5	3.9	503	2	A40583	heat shock transcr
1355	85.5	3.9	506	2	A33416	nuclear factor I -
1356	85.5	3.9	529	2	AD1042	hypothetical prote
1357	85.5	3.9	543	2	T22585	hypothetical prote
1358	85.5	3.9	544	2	S44814	F44B9.3 protein -
1359	85.5	3.9	574	2	AD1863	cobalamin biosynth
1360	85.5	3.9	576	2	T38293	hypothetical serin
1361	85.5	3.9	595	2	G64529	outer membrane pro
1362	85.5	3.9	601	1	B56564	transcription fact
1363	85.5	3.9	623	2	T28051	hypothetical prote
1364	85.5	3.9	633	2	T48786	tRNA-splicing endo
1365	85.5	3.9	634	2	T49415	hypothetical prote
1366	85.5	3.9	636	2	T38010	hypothetical prote
1367	85.5	3.9	678	2	JC4245	transcription fact
1368	85.5	3.9	681	2	T39950	cell cycle inhibit
1369	85.5	3.9	706	2	I52586	B-cell CLL/lymphom
1370	85.5	3.9	721	2	E70766	hypothetical prote
1371	85.5	3.9	731	2	B86369	hypothetical prote
1372	85.5	3.9	733	2	C64675	outer membrane pro
1373	85.5	3.9	770	2	G88445	protein C26E6.2 [i
1374	85.5	3.9	792	2	T21276	hypothetical prote
1375	85.5	3.9	796	1	JV0107	glucose dehydrogen
1376	85.5	3.9	796	2	H85495	glucose dehydrogen
1377	85.5	3.9	796	2	H90644	glucose dehydrogen
1378	85.5	3.9	856	2	C85023	hypothetical prote
1379	85.5	3.9	890	2	E81576	translation initia
1380	85.5	3.9	890	2	E86530	initiation factor-
1381	85.5	3.9	890	2	F72093	translation initia
1382	85.5	3.9	891	2	T40503	protein kinase kin
1383	85.5	3.9	904	2	S69691	hypothetical prote
1384	85.5	3.9	940	2	S19702	fibronectin-bindin
1385	85.5	3.9	964	2	T41547	hypothetical prote
1386	85.5	3.9	1018	2	T40253	hypothetical prote
1387	85.5	3.9	1047	2	A59246	HIRA protein - fru
1388	85.5	3.9	1079	1	TVFVMI	gag-Rmil-env polyp
1389	85.5	3.9	1095	2	T00329	hypothetical prote
1390	85.5	3.9	1160	2	T13713	beta3 protein - fr
1391	85.5	3.9	1173	2	T31421	C-terminal domain-
1392	85.5	3.9	1304	1	A46546	leukocyte common a
1393	85.5	3.9	1305	2	T23314	hypothetical prote
1394	85.5	3.9	1742	2	T49451	kinesin-like prote
1395	85.5	3.9	1828	2	A40115	microtubule-associ
1396	85.5	3.9	1844	1	RRWPTM	genome polyprotein
1397	85.5	3.9	1920	2	T13893	gene hindsight pro
1398	85.5	3.9	2176	2	T13806	toucan gene protei
1399	85.5	3.9	3305	2	T18358	apolipophorin prec
1400	85.5	3.9	215	2	S55925	probable arabinoga
1401	85	3.8	276	2	S36454	porin por1 - garde
1402	85	3.8	328	2	JQ0985	hydroxyproline-ric
1403	85	3.8	350	2	I38403	neu differentiatio
1404	85	3.8	390	1	C84347	hypothetical prote
1405	85	3.8	394	1	A47627	glycoprotein D pre
1406	85	3.8	407	2	G96835	probable RING zinc
1407	85	3.8	407	2	S52243	p46Eg265 protein -
1408	85	3.8	408	2	S39872	45 kDa protein - M
1409	85	3.8	425	2	T43454	hypothetical prote
1410	85	3.8	440	2	S69840	TyA protein - yeas
1411	85	3.8	478	2	A32555	major merozoite su
1412	85	3.8	493	2	T29833	hypothetical prote
1413	85	3.8	540	2	T27400	hypothetical prote
1414	85	3.8	544	2	S42723	matricin - mouse
1415	85	3.8	558	1	A39633	transcription fact
1416	85	3.8	572	2	T51525	hypothetical prote

Rank	%	Score	Accession	Length	DB	Description
1417	85	3.8	A35847	595	2	Fos-related antige
1418	85	3.8	T02795	598	2	probable membrane
1419	85	3.8	G87496	609	2	peptidase, M23/M37
1420	85	3.8	S19150	628	2	hypothetical prote
1421	85	3.8	F96660	635	2	protein F2K11.10 [
1422	85	3.8	T16078	645	2	hypothetical prote
1423	85	3.8	T02643	646	2	hypothetical prote
1424	85	3.8	T34082	687	2	s-layer protein -
1425	85	3.8	T18263	688	2	hypothetical prote
1426	85	3.8	E86790	725	2	regulatory protein
1427	85	3.8	C87432	756	2	Smoothened protein
1428	85	3.8	JS0747	788	2	myosin-light-chain
1429	85	3.8	JC5539	793	2	hypothetical prote
1430	85	3.8	JG0197	815	2	Scd1 protein - fis
1431	85	3.8	AB1841	826	2	glycoprotein B - b
1432	85	3.8	T37789	872	2	hypothetical prote
1433	85	3.8	S25530	874	2	hypothetical prote
1434	85	3.8	B97566	912	2	conserved hypothet
1435	85	3.8	T52517	929	2	dsRNA adenosine de
1436	85	3.8	T49038	964	2	hypothetical prote
1437	85	3.8	AH2786	1008	2	hypothetical prote
1438	85	3.8	T30340	1124	2	myosin IC - slime
1439	85	3.8	G87284	1145	2	atrophin-1 - human
1440	85	3.8	T21557	1162	2	atrophin-1 - human
1441	85	3.8	T30578	1181	2	protein kinase SK2
1442	85	3.8	S50832	1184	2	hypothetical prote
1443	85	3.8	G01763	1184	2	cell surface prote
1444	85	3.8	T34021	1206	2	cell surface prote
1445	85	3.8	T17479	1336	2	hypothetical prote
1446	85	3.8	AH1115	1348	2	dextransucrase (EC
1447	85	3.8	AI1476	1349	2	ZMS1 protein - yea
1448	85	3.8	T19188	1370	2	hypothetical prote
1449	85	3.8	JT0345	1375	2	bullous pemphigoid
1450	85	3.8	S57150	1380	2	guanine nucleotide
1451	85	3.8	A46053	1433	2	proliferation pote
1452	85	3.8	BVBYX1	1435	2	ras-responsive ele
1453	85	3.8	T42727	1560	2	phosphodiesterase
1454	85	3.8	JC6510	1615	2	TyB protein - yeas
1455	85	3.8	T30244	1687	2	genome polyprotein
1456	85	3.8	S69839	1755	2	sdk protein - frui
1457	85	3.8	RRWPEM	1839	2	beta-galactosidase
1458	85	3.8	T13924	2222	2	adenylate cyclase
1459	85	3.8	B95075	2233	2	notch homolog - se
1460	85	3.8	D42088	2248	2	suface antigen - P
1461	85	3.8	T31070	2531	2	probable guanine n
1462	85	3.8	T31687	2543	2	tail fiber protein
1463	85	3.8	T09144	2559	2	merozoite surface
1464	84.5	3.8	A41883	253	2	glutamate racemase
1465	84.5	3.8	S01704	259	1	hypothetical prote
1466	84.5	3.8	A49473	268	2	histone H1 - commo
1467	84.5	3.8	T01612	281	2	leucocyte common a
1468	84.5	3.8	S53502	282	2	regulatory protein
1469	84.5	3.8	A45854	287	2	hypothetical prote
1470	84.5	3.8	A35630	340	2	hypothetical prote
1471	84.5	3.8	T29315	385	2	phaseolin type alp
1472	84.5	3.8	T20327	417	2	ARIF-1 orf20/21 -
1473	84.5	3.8	A23498	436	2	hypothetical prote
1474	84.5	3.8	T41766	440	2	microtubule-associ
1475	84.5	3.8	D81716	445	2	hypothetical prote
1476	84.5	3.8	I67793	472	2	conserved hypothet
1477	84.5	3.8	T32938	477	2	hypothetical ser-p
1478	84.5	3.8	F81655	491	2	nucleoporin-like p
1479	84.5	3.8	T39092	551	2	probable membrane
1480	84.5	3.8	A57088	562	2	proline-rich prote
1481	84.5	3.8	S66710	573	2	calcium binding PW
1482	84.5	3.8	T19061	584	2	polymyxin B resist
1483	84.5	3.8	S62057	633	2	hypothetical prote
1484	84.5	3.8	JC4248	634	2	hypothetical prote
1485	84.5	3.8	S56909	668	2	hypothetical serin
1486	84.5	3.8	T19703	679	2	rna14 protein - fi
1487	84.5	3.8	T25603	684	2	
1488	84.5	3.8	T41586	710	2	
1489	84.5	3.8	T11668	733	2	
1490	84.5	3.8	T26006	736	2	hypothetical prote
1491	84.5	3.8	S17925	740	2	polynucleotide ade
1492	84.5	3.8	A49672	742	2	transcription fact
1493	84.5	3.8	AB1452	756	2	chitinase B homolo
1494	84.5	3.8	AI2639	757	2	cheA homolog [impo
1495	84.5	3.8	B97422	757	2	chea homolog (AF04
1496	84.5	3.8	T38929	775	2	changed division r
1497	84.5	3.8	B71478	799	2	probable cell divi
1498	84.5	3.8	JC7113	803	2	cyokinesis initia
1499	84.5	3.8	S33708	808	1	nuclear steroid/th
1500	84.5	3.8	I78885	841	1	serine/threonine-s

ALIGNMENTS

RESULT 1
T29634
hypothetical protein C12D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T29634
R;Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C12D12.
A;Reference number: Z20656
A;Accession: T29634
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-825 <NHA>
A;Cross-references: UNIPROT:Q17921; UNIPARC:UPI000017847E; EMBL:U51998; PIDN:AAA96080.1
A;Experimental source: strain Bristol N2; clone C12D12
C;Genetics:
A;Gene: CESP:C12D12.1
A;Map position: X
A;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1

Query Match   7.9%; Score 174.5; DB 2; Length 825;
Best Local Similarity 23.7%; Pred. No. 0.00054;
Matches   93; Conservative   40; Mismatches 144; Indels 115; Gaps   17;

```
Qy    52 NEPVYTSTQED----CINSCCSTKNISGDKACNLMIPDTRK------------ 88
                        |: |: |||:
Db   363 NTPFFTRNANDTIEIYCTVLSCSSITIDGVK---IQITDTKVVQKVDDISYYIFVNTIAN 419

Qy    89 ----TARQPNCYLFFC---------PNEEACPLKP--AKGLMSY--RIITDF 123
                            |:  |||
Db   420 PGYHQISLKQQGSYAFFVYGKNKLYSGYEGGANKPTVVLAPPTTPGPTFYPVTTVSTMS 479

Qy   124 PSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLE 183
         |:
Db   480 PPTTVTVPTTPTVP-------TTTNTPPANPTT--ATPTTVG---TSKQTNTISPHLS 526

Qy   184 KLFKMDEASAQLLAYKEKG-------HSQSSQFSSDQEIAHLLPENVSALPATVAVASPH 236
              :                      |:  :| :
Db   527 TIITGSIVTSTPTMAPQTSASPTTTPTHTTASQPTTTKPV--VTTNSVTPSTGTTTVPVP- 583

Qy   237 TTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQA 296
         ||:  ::      :      ||||||||||  ::
Db   584 TTTGSPTTQTTAPVTKPTVPSSTTQ----TAPPVTTPTSQPPVTTTSLLTTLTTPTVPV 638

Qy   297 MAT------------TAVLTTTPQA-------------PTDSKGSLETIPFT 323
         ||:            : |||::||             |:
Db   639 TTTVVPSSATVPTTPPTTVTVAATTTSKAPVVTTSPTLAPTSPTKLPTSPPSTVGTSP-T 697

Qy   324 EISNLTLNTGNVYNPTALSMSNVESSTMNKTA 355
                  ::  |||
Db   698 APANLTTPTTAPVNPT--SSTTAPTAPVNPTS 727
```

RESULT 2
S53362
mucin 5AC (clone JER47) - human (fragment)

```
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S53362; S71065
R;Guyonnet-Duperat, V.; Audie, J.P.; Deballleul, V.; Laine, A.; Buisine, M.P.; Galiegue-
Biochem. J. 305, 211-219, 1995
A;Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich doma
A;Reference number: S53361; MUID:95126907; PMID:7826332
A;Accession: S53362
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-477 <GUY>
A;Cross-references: UNIPROT:Q14887; UNIPARC:UPI000017C2A9; EMBL:Z34277
A;Experimental source: clone JER47
R;Porchet, N.
submitted to the EMBL Data Library, June 1994
A;Reference number: S71065
A;Accession: S71065
A;Molecule type: mRNA
A;Residues: 1-211,'S',213-224,'AR',227-259,'S',261-477 <POR>
A;Cross-references: UNIPARC:UPI00006D4B3; EMBL:Z34277; NID:g563374; PIDN:CAA84031.1; PI
A;Experimental source: clone JER47
C;Genetics:
A;Gene: GDB:MUC5AC
A;Cross-references: GDB:454136; OMIM:158373
A;Map position: 11p15.5-11p15.5
C;Keywords: glycoprotein; tandem repeat

Query Match          7.3%;    Score 160.5; DB 2;   Length 477;
Best Local Similarity   23.8%;   Pred. No. 0.0024;
Matches    76;  Conservative    41;  Mismatches   117;  Indels    85;  Gaps    13;

Qy   147 SQAVTPLAHHHTDYSKPTDISW--------RDTLSQKFGSSDHL----BKLFKMD----  189
             ::| :||            : : :::     : ::.::
Db    15 SQPVTRDCHLRCTWTKWFDVDFPSPGPHGGDKETYNNIIRSGEKICRRPEEITRLQCRAE  74

Qy   190 ---EASAQLLAY-----KEKG-----HSQSSQFSS--DQEIAHLLPENVSALPATVAVAS  234
            :| |             :::|           : :|         ::   ST 131
Db    75 SHPEVSIEHLGQVVVQCSREGLVCRNQDQQGPFKMCLNYEVRVLCCETPKGCPVT---ST  131

Qy   235 PHTTSATPKPATLLPTNAS--------------VTPSGTSQPQLATTAPPVTTVTSQPPTLI  283
             : :|| :||||||:|||               ||:| :|||||||:|:|:|||:| :
Db   132 PVTAPSTPSGRATSPTQSTSSWQKSRTTLVTTSTTSTPQTSTTSAPTTSTTSAPTTSTT  191

Qy   284 STVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLET-------------IPFTEISNLTL  330
             | |:|||||||||||||:||||||||:|||| :||              |||||:|:|
Db   192 SAPTTSTTSTPQTSISSAPTTSTTSAPTTSTTSRATTSIISAPTTSTTSFPTTSTTSAT  250

Qy   331 NTGNVYNPTALSMSNVE------SSTMNKTASWEGREASP-------GSSSQGSVPEN  375
             :||:||||||:|:|||        :.|::||::|||:|||           :| ||
Db   251 TTSTTSAPTTSTTSTPQTSKTSAATSSTTSGSGTTPSPVTTSTASVSKTSTSHSVSKT  310

Qy   376 QYGLP----------FEKW 384
             :|:||           ||
Db   311 THSQPVTRDCHPRCTWTKW 329

RESULT 3
T22808
hypothetical protein F56H9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22808
R;Burton, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19618
A;Accession: T22808
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <WIL>
A;Cross-references: UNIPROT:Q20908; UNIPARC:UPI000000831C3; EMBL:Z74473; PIDN:CAA98949.1;
A;Experimental source: clone F56H9
C;Genetics:
A;Gene: CESP:F56H9.1
```

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A;Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Query Match          7.0%;    Score 155.5; DB 2;   Length 770;
Best Local Similarity   32.7%;   Pred. No. 0.0095;
Matches    48;  Conservative    16;  Mismatches    64;  Indels    19;  Gaps     5;

Qy   219 LPENVSALPATVAVASPHTTSATPKPATLLPTNASVT-----PSGTSQPQLATTAPPV--  271
             | : | |: |:| ::|  ::|:::::|:::|        |:|| :| :
Db    93 VPPTTSTTTTTTV--PPTTTSTTTTTVPPTTTSSTTTTVPPTTTSTTTTTVPPTTT  150

Qy   272 --TTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLT  329
             :|.||  : |::        :: :| |  ::|          ::|||:|:|:||:|:
Db   151 TSTTTTVPPTTTSTTTTTTT-----TTSTATTTTVPPTTTSTTTTTVPPTTTSTT  205

Qy   330 LNTGNVYNPTALSMSNVESSTMNKTAS  356
             ::||                :::|::
Db   206 TTT---VPPTTTSSTTTTTTTLPTTT  229

RESULT 4
T22696
hypothetical protein F55B11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22696
R;Ainscough, R.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19601
A;Accession: T22696
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-851 <WIL>
A;Cross-references: UNIPROT:O17893; UNIPARC:UPI0000001641DA; EMBL:Z83318; PIDN:CAB05903.1;
A;Experimental source: clone F55B11
C;Genetics:
A;Gene: CESP:F55B11.3
A;Map position: 4
A;Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3

Query Match          7.0%;    Score 154.5; DB 2;   Length 851;
Best Local Similarity   26.6%;   Pred. No. 0.013;
Matches    47;  Conservative    26;  Mismatches    89;  Indels    15;  Gaps     4;

Qy   219 LPENVSALPATVAVAS------PHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVT  272
             | : || |: |:|        |:||  ::|:|::: |:|   : |
Db   377 VPTTTTTVPTTTTTVSTTTTTVPTTTTTVPTTTTTVPTTTTTVPTTTVPTT  436

Qy   273 TVTSQPPTTLISTVFTRAAATLQAMA--TTAVLTTTFQAPTDS---KGSLETIPFTEIS-  326
             |:||              :: :| |   |::|         |      :::|||:|:|
Db   437 TTTVPTTTTTVSTTTTTVSTTTTTVPTTTTTTTVPTTTTTVPTTTTTSV  496

Qy   327 ---NLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSSQGSVPENQYGLP  380
             .: ::|::||                    :::|:|:
Db   497 PTTTTVPTTTTTVPTTTTTVSTTTTTVPTTTTTVPTTTTTVSTTTTTVPTTTTTVP  553

RESULT 5
T39903
serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39903
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21889
A;Accession: T39903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-534 <LYN>
A;Cross-references: UNIPROT:O94317; UNIPARC:UPI0000069AEB; EMBL:AL033534; PIDN:CAA22127
A;Experimental source: strain 972h-; cosmid c215
C;Genetics:
```

A;Gene: SPDB:SPBC215.13
A;Map position: 2
C;Superfamily: pig submaxillary mucin

Query Match   7.0%; Score 154; DB 2; Length 534;
Best Local Similarity 21.1%; Pred. No. 0.0075;
Matches   86; Conservative   79; Mismatches 183; Indels   60; Gaps   13;

Qy   9 LYTYLVII--------CFLTLRLSASQNCLKKSLEDVV-IDIQSSLSK--GIR------ 50
            |:::|:: |:   :::::|: :::::: ::: ::: :::
Db   5 LLPSLICVFCISNIFTQAFLVHQIYGNSSFTKISLNQLEGRDSQEELQRRQEIRYYGRAA 64

Qy   51 --GNEPVY------TSTQEDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCP- 101
            ::: |:   :: : |: :: :::: ::: : :: ::|: ::::
Db   65 ETGGTPTYYGYATPTSSSEPSIFSESATPSETNSYSSPVSSYSDPATSQLPSSTSFFSPT 124

Qy   102 ----NEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGGPSQAVTPL 153
              :|: | : ::|: :::: : : :: :::|:::::|: :: |: :
Db   125 SSEYTPSSTESSSLLDPSS--VSSAILPSSTSVEVSISSSLSSSSDPLTSSTFSSLSS-- 180

Qy   154 AHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQ 213
          ::|: |::::|:::::::::: ::|: ::: ::::::::::::::::::: :::::: :|
Db   181 ---STSSSQP---SVSSTSSSTFSSAAPTSTSSSYLSSSSVVSSSSSPSSSSSSTLTSSS 234

Qy   214 EIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPLATTAPPVTT 273
          :::: : : ::: : : :::: :: : :::
Db   235 LSTSSIPSTSSSSSTSSSLSSSSSTASSSSSSSSSSSPPTSTSSTISSSS 294

Qy   274 VTSQOPPTTLISTVFTRA------AATLQAMATTAVLTTTF-QAPTDSKGSLETIPFTEIS 326
            |::: ::: ::::::   ::: :: :: ::::: :|:::::::::::::::::
Db   295 SSSSSPTSTSSTISSSSSSSFSSTLSSSMSS--SSFSSSPTSSWGREASPGSSS 352

Qy   327 NLTLNT------GNVYNPTALSMSNVESSTMNKTASWEGREASPGSSS 368
          :: ::   :::: ::::::::::: :::: ::::
Db   353 SSFSSTTSSSKSSSSFSSTVSSSSSSTVSSSSSSTLTSSSSSSRPASSSSHS 400

RESULT 6
T21389
hypothetical protein F26C11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21389
R;Matthews, P.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19416
A;Accession: T21389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1251 <WIL>
A;Cross-references: UNIPROT:Q09550; UNIPARC:UPI000013BF4C; EMBL:Z47072; PIDN:CAA87369.1;
A;Experimental source: clone F26C11
C;Genetics:
A;Gene: CESP:F26C11.3
A;Map position: 2
A;Introns: 24/1; 111/1; 208/1; 272/1; 380/1; 394/3; 485/3; 586/3; 630/3; 669/3; 713/3; 7

Query Match   6.9%; Score 151.5; DB 2; Length 1251;
Best Local Similarity 22.4%; Pred. No. 0.033;
Matches   93; Conservative   46; Mismatches 161; Indels 115; Gaps 17;

Qy   17 CFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCI---------- 64
          |::::|::::: ::|: ::::::|:|:::::: :
Db   82 CDCVLTSSSSTETGTVKPLDREFRRVFSSAEIASTTSLPTTTSPSLNCYWLSEPSNFSEWI 141

Qy   65 --------NSCCSTKNI---SGDKACNLMIFDTRKTARQPNCY--LPFC-PNEEACP 107
                   :| :::   :::::::::::::::::::::: : |: :|::: |
Db   142 DGKQTNLRYNGGCCSETSIQVLNSSDS--TRWILTTSDSWNKANALINLLYCTPN--ACP 197

Qy   108 LKPAKGLMSYRIITDPPSLT----RNLPSQELPQEDSLLHGGPSQAVTPLAHHHTDVSKP 163
          |: :|::::|::::: |:| |::|:::::|:::::::| : : ::::|: :::
Db   198 QQSMLWTNCSNLSTTTSSSSTMLSSTTLLTTETRESSSTGS-TQTTTPSTEPSTTITTP 256

164 TDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENV 223
Qy   :
Db 257 ME--QSSTVSS---------- 265

Qy 224 SALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
          : : ::: ::: :::::|:: ::: :|:::::: :::: :::|: : :
Db 266 --------VQKTRTSEDKPSSSTVVPTSAASTSESSSTSSP-MAETSSSSTTSQSSPAST-- 314

Qy 284 STVFTRAAATLQAMATTAV--LTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTAL 341
          :||:   :::: ::: ::: :::::::::|: :::: ::: :: : ::: :::
Db 315 STV--PESSTVGSTPTTGLTTLSTNEQSTSTSSGGHSTSTPFSGTTSE-TPETSTDFTATST 371

Qy 342 S-------MSNVESSTMNKTASWEGREA$PGSSSQGSVPENQYGLPF--EKWLL 386
          | :::::::::::
Db 372 SSSDDSSTQSSNAQTSTIENGSTTTNFTSAPSTSSTTPATPTTTYNWPTGGTTWML 426

RESULT 7
VGBEX1
glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p)
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: H36802
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A;Description: The DNA sequence of equine herpesvirus-1.
A;Reference number: A36805
A;Accession: H36802
A;Molecule type: DNA
A;Residues: 1-797 <TEL>
A;Cross-references: UNIPROT:P28968; UNIPARC:UPI000013B750; GB:M86664; NID:g330791; PIDN:
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:92295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Genetics:
A;Gene: 71
C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein homo
C;Keywords: glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-797/Product: glycoprotein X #status predicted <MAT>
F;23-465/Region: serine/threonine-rich
F;489-797/Domain: equine herpesvirus 1 glycoprotein homology <EHG>
F;766-790/Domain: transmembrane #status predicted <TMN>
F;590/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   6.8%; Score 150.5; DB 1; Length 797;
Best Local Similarity 24.3%; Pred. No. 0.021;
Matches   58; Conservative   25; Mismatches 131; Indels   25; Gaps   2;

Qy 158 TDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAH 217
          |:::||||||||||||||:|||||||||||||||||||||::||||||||||:::::
Db   29 TTSSSTSGSGQSTSSGTTNSSSSPTTSPPTTSSSPPSTSTHTSSSPSSTSQSSTSATSS 88

Qy 218 LLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTP---------------- 256
          |||:::::: :
Db   89 SAPSTASSTTSIPTSTSTETTTTTPTASTTTPTTTPTTTTAAPTTATTAVTTAASTSAETTT 148

Qy 257 ---SGTSQPQLAT-TAPPVTTVTSQPPTTLISTVFTRAAAATLQAMATTAVLTTTFQAPTD 312
             :|: : :: ::::::::   ::
Db 149 ATATATSTPTTYTPTSTTTTPTSTTTTATTIVPTTASTTDTTTAATTTAATTTAATTTAA 208

Qy 313 SKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSSQGS 371
          :|:||||:
Db 209 TTTAATTTAATTTAATTTAATTSSATTAATTTAATTTAATTTAATTTAATTTTGSPTSGS 267

RESULT 8
JC4566
chitinase (EC 3.2.1.14) 2 precursor - Coccidioides immitis

N;Alternate names: chitin hydrolase homolog; CTS2 protein
C;Species: Coccidioides immitis
C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
C;Accession: JC4566
R;Pishko, E.J.; Kirkland, T.N.; Cole, G.T.
Gene 167, 173-177, 1995
A;Title: Isolation and characterization of two chitinase-encoding genes (cts1, cts2) fro
A;Reference number: JC4565; MUID:96144270; PMID:8566773
A;Accession: JC4566
A;Molecule type: mRNA
A;Residues: 1-860 <PIS>
A;Cross-references: UNIPARC:UPI000017B3AE; GB:L41662
C;Genetics:
A;Gene: cts2
A;Introns: 35/3; 181/2
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;22-239/Domain: catalytic #status predicted <CAT>
F;23-860/Product: chitinase 2 #status predicted <MAT>
F;346-682/Region: serine/threonine-rich
F;687-860/Region: cysteine-rich
F;90,657/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match      6.8%;   Score 150.5;  DB 2;  Length 860;
Best Local Similarity  23.9%;  Pred. No. 0.024;
Matches   78;  Conservative  49;  Mismatches 141;  Indels  59;  Gaps  12;

Qy   65 NSCCSTKN-ISGDKACNLMIFDTRKTARQ---PNCYLFFCPNEEACPLKPAKGLMSYRII 120
         ||  |||  :||: |:   |:   | ||          | | ||| | :| |   |
Db  235 NPSCSAKRWVTNPKSVTYTVDDWVKYIRKSGNPLAKLFI----------------------- 273

Qy  121 TDFPSLTRNLPSQE--LPQEDSLLHGQFSQAV-TPLAHHHTDYSKPTDISWRDTLSQ--K 175
Db  274 --------GLPASKSAAAKEDYLTPGEATKIVSTYMAKYPSTFGGM--MVWEATASENNK 323

Qy  176 FGSSDHL---EKLFKMD--EASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPA 228
Db  324 LGGLPYADIMKEVLLRCDPDPFSTVTSTTSASTSTQTSSQSTTMETKTLSASTTPSSPS 383

Qy  229 TVAVASPHTTSATPKPATLLPTNASVTPSGTSGQPQLATTAPPVTTVTSQPPTTLISTVFT 288
Db  384 TVSPSSTMQTTSTGSTSIETVTTRSQEPPSTTISTRSASTEPVTTRSQEPPSTTIS---T 440

Qy  289 RAAA----TLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLTNTGNVVNPTALSMS 344
Db  441 RSASTETVTTRSQEPPSTTISTWSASTETSTSSQDSPSTTISTKSAPTG-----TVTTRS 495

Qy  345 NVESSTMNKTASWEGRASPGSSSQGS 371
Db  496 QDLPSTTISTRSPETETETATTKSQGS 522
```

RESULT 9
A43932
mucin 2 precursor, intestinal - human (fragments)
N;Alternate names: mucin SMUC-41
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 31-Dec-2004
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the
A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963
A;Molecule type: mRNA
A;Residues: 1-639 <GU1>
A;Cross-references: UNIPROT:Q02817; UNIPROT:Q02817; UNIPROT:Q14884; UNIPARC:UPI0000177AE0; GB:L21998
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S.
J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MUC2 mucin gene has cysteine-rich subdomains located both upstr
A;Reference number: A45106; MUID:93016075; PMID:1400449
A;Accession: A45106
A;Status: not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 626-1895 <GU2>
A;Cross-references: UNIPARC:UPI00016AB12; GB:M94131; NID:g186395; PIDN:AAA59163.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIP:116706)
A;Accession: B45106
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 2037-3020 <GU3>
A;Cross-references: UNIPARC:UPI00016AB13; GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:
A;Experimental source: colon
A;Note: sequence extracted from NCBI backbone (NCBIP:116698)
R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.M
J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorp
A;Reference number: A43932; MUID:91358717; PMID:1185763
A;Accession: A43932
A;Molecule type: DNA
A;Residues: 1343-1350,'I',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
A;Cross-references: UNIPARC:UPI00016AD85; GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:55749, NCBIP:55750)
R;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden
A;Reference number: A33532; MUID:89197956; PMID:2703501
A;Accession: B33532
A;Molecule type: mRNA
A;Residues: 1916-2193 <GU4>
A;Cross-references: UNIPARC:UPI0000731C8; GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:
A;Experimental source: intestine
R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.
J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin gene.
A;Reference number: A61257; MUID:91086481; PMID:1985113
A;Accession: A61257
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
A;Cross-references: UNIPARC:UPI0000177AE1
A;Experimental source: bronchus
R;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner,
Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t
A;Reference number: PQ0328; MUID:92198477; PMID:1550588
A;Accession: PQ0328
A;Molecule type: mRNA
A;Residues: 2328-2468 <XUG>
A;Cross-references: UNIPARC:UPI0000177AE2; GB:M86523
A;Experimental source: small intestine
A;Accession: PQ0329
A;Molecule type: protein
A;Residues: 2328-2342,'K',2344-2354 <XUG1>
C;Genetics:
A;Gene: GDB:MUC2
A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor type C repeat homology
C;Keywords: glycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>

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Query Match      6.8%;   Score 149.5;  DB 2;  Length 3020;
Best Local Similarity  34.1%;   Pred. No. 0.14;
Matches   43;  Conservative  12;  Mismatches  52;  Indels  19;  Gaps   4;

Qy  220 PENVSALPATVAVASPHTTSATPKPATL--LPTNASVTP--SGTSQPQLATTAPPVTTVT 275
                                        :|:|||:|||  :||     | |    | |:|
Db 1511 PASTTLPPTTTPSPPTTTTTTTPPPTTTTSTTTLPPTTTPSPPTTTTT 1570

Qy  276 SQPPTTLIS----------TVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFT 323
         ::|||                                                  |||
Db 1571 TPPPTTTTPSPPTTTTPSPPTTTTTTPPPTTTSPPTT---TTTTPPPTTTPSPPTTPIT 1627
```

```
Qy      324 EISNLT 329
            ::||||
Db     1628 PPTSTT 1633

RESULT 10
T45025
mucin MUC5B, tracheobronchial [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat
A;Reference number: Z22899; MUID:97166151; PMID:9013550
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: UNIPARC:UPI000016AD88; EMBL:Z72496; PIDN:CAA96577.1; NID:g1834502; E
A;Experimental source: placenta
C;Genetics:
A;Gene: MUC5B

Query Match        6.8%;    Score 149.5;  DB 2;  Length 3570;
Best Local Similarity   30.5%;  Pred. No. 0.17;
Matches    62;  Conservative    22;  Mismatches    58;  Indels    61;  Gaps    10;

Qy      204 SQSQFSSDQEIAHLLPENVSALPATVAVA-SPHTTSATPKPATLLPTNASVTPSGTSQP 262
                |:||       ::|||||:||:|:|: :||         ||:|||||:||||||||||
Db      626 SKATPFSS--------PGTATALPALRSTATTPTATSFTAIPSSSL---------GTTWT 668

Qy      263 QLATTAPPVTTV-----TSQPPTTLISTVFTVTRAAATLQAMA-------------TTAVLT 304
                :|:|:       :|||||| |||:|:| :| :||||||                ||||
Db      669 RLSQTTTPMATMSTATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTPGTAHTTKVLT 728

Qy      305 TT---FQA-PTDSKGSLETIPFTEISNLTLNT----------GNVYNPTALSMSNVES 348
                ||   || |     |:|: :|:|:|||||            ::|||:||:| |::|
Db      729 TTTTGFTATPSSSPGRARTLP-VWISTTTPFTTRGSVTVTPSSIPGTHTPTVLTTTTTTV 787

Qy      349 STMNKTASWEGREASPGSSSQGS 371
                ||           :|:|||||
Db      788 AT------GSMATPSSSTQTS 802

RESULT 11
T34293
hypothetical protein F49E10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34293
R;Miller, N.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F49E10.
A;Reference number: Z21500
A;Accession: T34293
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-790 <MIL>
A;Cross-references: UNIPROT:Q20599; UNIPARC:UPI000007D415; EMBL:US3341; PIDN:AAC69106.1;
A;Experimental source: strain Bristol N2; clone F49E10
C;Genetics:
A;Gene: CESP:F49E10.2
A;Map position: X
A;Introns: 51/1; 92/3; 176/3; 235/3; 332/2; 514/1; 543/2; 569/3; 677/1; 732/3

Query Match        6.7%;    Score 147.5;  DB 2;  Length 790;
Best Local Similarity   25.6%;  Pred. No. 0.034;
Matches    60;  Conservative    34;  Mismatches   107;  Indels    33;  Gaps    11;

Qy      152 PLAHHHTDYSKPTDISWRDTLSQKF--GSSDH--LEKLFKMDEASAQLLAYKEKGHSQSS 207
                |:|||||||||||    ::|       ||||  :|| | ||     ||: |    ::|:
Db      537 PFGFHNRPFSK-KDLG---LPEGFQVGQSQYRPIEK--KQGFATLPLRKVSTVPPTTST 589
```

Right column:

```
Qy      208 QFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATT 267
                ::| :|         :||||||||||||||||||||||||||||||||          |
Db      590 SSTTTQK------PSTTTTVPSTTPTSTTTTTTTPIPKPTTSTSTSTTTTTTTTSTTAVTT 644

Qy      268 APPVTTVTSQPPTTLISTVFTVTRAAATLQAMATTAVLTTTFQA-------PTDSKGSLETIPF 322
                ||||||||||||||||||||||||||||||:|| ||:| :|  |       |:|:||||||:
Db      645 PQPTTTTTSEKPVTLTTQTWTAPPTTVKRTTPQTVPTTTPKIPRWWPLAGSGSTEQ-PW 703

Qy      323 TEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREA2PGSSSQGSVPENQ 376
                |:|:|:|||||||||||||||||||||||||||||||||||        ||:|||||
Db      704 WQ---KVQTGQNTLPPLFPVSKRVEEKVEKVS------AKP-NESDNKIPEQK 746

RESULT 12
S25345
probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCR1102
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S25345; S19504
R;Wilson, C.; Grisanti, P.; Frontali, L.
Yeast 8, 569-575, 1992
A;Title: The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromos
A;Reference number: S25345; MUID:92397594; PMID:1523889
A;Accession: S25345
A;Molecule type: DNA
A;Residues: 1-1609 <WIL>
A;Cross-references: UNIPROT:P25653; UNIPARC:UPI000012A7A9; GB:X59720; EMBL:S43845; NID:9
R;Frontali, L.; Grisanti, P.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19504
A;Accession: S19504
A;Molecule type: DNA
A;Residues: 1-1609 <FRO>
A;Cross-references: UNIPARC:UPI000012A7A9; EMBL:X59720; NID:g1907116; PID:e264634; PID:9
C;Genetics:
A;Gene: SGD:FIG2
A;Cross-references: SGD:S0000685; MIPS:YCR089w
A;Map position: 3R
A;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;1592-1609/Domain: transmembrane #status predicted <TM2>

Query Match        6.7%;    Score 147.5;  DB 2;  Length 1609;
Best Local Similarity   22.4%;  Pred. No. 0.083;
Matches    88;  Conservative    63;  Mismatches   164;  Indels    77;  Gaps    14;

Qy       41 IQSLSKGIRGNEPVTTSQEDCINSCCSTKNISGDKACNLMIFDTR----KTARQPNCY 96
                |||||           ||:|::             :|            ||
Db     1057 IMSSSSNVISTNEKPSSTTSPYNFSSGYSLPSSTPSQYSLSTATTTINGIKTV----Y 1111

Qy       97 LFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHH 156
                |:  ||       |: ||| :|:||| :|| ||| :| |||::    | : :||
Db     1112 TTWCPLAEKSTV--AASSQSSRSVDRFVSSSK--PSSSLSQ--TSIQVTLSTATTTISGL 1165

Qy      157 HTDYSKPTDISWRDTLSQKFGSSDHLE-KLFKMDEASAQLLAYKEKGHSQSSQ----F 209
                |||:|||||||||||||||        ||||||||||||||||||||||||        :
Db     1166 KTVYTTWCPLTSKSTLGATTQTSSTAKVRITSASSATSTISLSTSTESESSSGYLSKGV 1225

Qy      210 SSDQEIAHLLPENVSALPATVAVASP-----------HTTSATPKPAT----LLPTNASV 254
                ||| :|          ||||||||||            |:|||:|||    ||   |:
Db     1226 CSGTECTQDVPTQ-SSSPASTLAYSPSVSTSSSSFSTTASTLTSTHTSVPLLPSSSSI 1284

Qy      255 TPSGTSQPQLATT---APPVTTVTSQPPTTLISTVFTVTRAAATLQAMA-------TTAVLT 304
                ||||||||||||    ||||||||||||||||||||||||||||||||        :||||
Db     1285 SASSPSSTSLLSTSLLSPSPAFTSSTLPTATAVSSSTFIASSLPLSSKSSLSPVSSSSIM 1344

Qy      305 TTFQAPTDSKGSLETIPFTBISNLLNTGNVYNPT----------------- 339
                ||:|||||||||||||||||:|:|:|||||||||
Db     1345 SQFSSSSSSSSSLASLPSLSISP-TVDTVSVLQPTTSIATLTCTDSQCCQQBVSTICNGSN 1403

Qy      340 ---ALSMSNVESSTMNKTASWEGREASPGSSS 368
```

```
Db    1404 CDDVTSTATTPPSTVTDTMTCTGSECQKTTSS 1435
               |||  :||  :|   |  :|   :||

RESULT 13
A45155
mucin FIM-C.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A45155
R;Hauser, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1
A;Reference number: A45155; MUID:93077556; PMID:1447205
A;Accession: A45155
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
A;Cross-references: UNIPROT:Q05049; UNIPARC:UPI000012F8CF; GB:L02115; NID:g214147; PIDN:
F;162-202/Domain: trefoil homology <TRF1>
F;354-394/Domain: trefoil homology <TRF2>
F;347-347/Domain: trefoil homology <TRF3>
F;526-566/Domain: trefoil homology <TRF4>
F;573-613/Domain: trefoil homology <TRF5>
F;621-661/Domain: trefoil homology <TRF6>

Query Match        6.6%;    Score 147;    DB 2;    Length 662;
Best Local Similarity  26.9%;    Pred. No. 0.029;
Matches   49;  Conservative   19;  Mismatches   78;  Indels   36;  Gaps   5;

Qy   228 ATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPLATTAPPVTT------VTSQPP 279
             :|| |:|:| |||:|:|:|::| |:| |:|:  |:|  ||:|      |:|
Db   394 STSQVAATKTT--TTPTTTTPTTTTTPTTTTTPTTTTTTTTTKATTTTPT 451

Qy   280 TTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPPFTEISNLTLNTGNVYNPT 339
             |:||  |||||||:|||||||||||||||||||||||  |:| ||||||||||||||
Db   452 TTTPTTTTTKATTTTPTTTTTPTTTTTTTPTTTTTKATTTT----PT 506

Qy   340 ALSMSNVESSTMNKTAS--------------WEGREASPGSSSQGSVPENQ---YG 378
             |||||||||||||||||              :|:|:::| :|:::| |:|:
Db   507 TTTTTTTTTKATTTTTTSGECKMEPSKRADCGYPGITESQCRSKGCCFDSSIPQTKWCFYS 566

Qy   379 LP 380
             ||
Db   567 LP 568

RESULT 14
A47547
serine proteinase stubble-stubbloid (EC 3.4.21.-) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A47547
R;Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds, A.; Garbe, J.C.; Fristrom, D.; Fris
Proc. Natl. Acad. Sci. U.S.A. 90, 4937-4941, 1993
A;Title: The Drosophila Stubble-stubbloid gene encodes an apparent transmembrane serine
A;Reference number: A47547; MUID:93281671; PMID:7685111
A;Accession: A47547
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-786 <APP>
A;Cross-references: UNIPROT:Q05319; UNIPARC:UPI000013615A; GB:L11451; NID:g158511; PIDN:
C;Genetics:
A;Gene: Sb-sbd
A;Cross-references: FlyBase:FBgn0003319
C;Superfamily: hydrolase; serine proteinase; trypsin homology
C;Keywords: transmembrane protein
F;61-77/Domain: transmembrane #status predicted <TMN>
F;543-781/Domain: trypsin homology <TRY>

Query Match        6.6%;    Score 146;    DB 1;    Length 786;
Best Local Similarity  21.0%;    Pred. No. 0.042;
Matches   74;  Conservative   47;  Mismatches  162;  Indels   70;  Gaps   9;
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Qy    63 CINS----CCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYR 118
             |::|    |:::  :|::|
Db   164 CVDSFMFGSCCTHNVTD---NIVLPQTAFSYTRPTKPLTLRPRPPAAPYKP-------- 211

Qy   119 IITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTD---------YSKPTDISW 168
             ||||:::|||:|:| ::|:| ::||||                          ||||
Db   212 ------MISGMTTIERP------HGAGTLVIRPSGPHHQGTLARPHPPPYQSKPT-- 254

Qy   169 RDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSAL-- 226
             |:|:||||:|||||||||||||||||||||||||||||||:||||  |:||:|||
Db   255 --TASDLHGSASHPSSSSSSSSSNPNSIWHTSTQQQQHQQNQQNHWQMTEPSFITK 312

Qy   227 -------PATVAVASPHTTS------------ATPKPATLLPTNASVTPSGTSQPQLA 265
                    |||:||||||||            ||||||||||||||:|:||||:|:|||
Db   313 PRPTGWTKPGIVNLPMPARPSKPSKPTKKPIVYDRSPPPPSSVPPSTSTSTSTSLIWPA 372

Qy   266 TTAPPVTTVTSQPPTLISTVFTRAAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEI 325
             |||:::|:|:|||| |:||:|||||:::|:|||||||||||||||:|||||:||||:|||
Db   373 QTHPQQPHRPTRPQLSPGTSLAASSSSHWPSSTSTTSSTTSSTSSTTTTTTTRRTTTPTTTT 432

Qy   326 SNLTLN--TGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSVPENQ 376
             |:|:|:  :| |:|| |:::|::::|:
Db   433 RRTTTNKPTRPYQRPTTATSSSSTSTTSSKTPTTTRPISSSSSSSSGIVTSSQ 485

RESULT 15
B46629
mucin 6, gastric (3-repeat clone) - human (fragment)
N;Alternate names: MUC6
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B46629
R;Toribara, N.W.; Roberton, A.M.; Ho, S.B.; Kuo, W.L.; Gum, E.; Hicks, J.W.; Gum Jr., J.
J. Biol. Chem. 268, 5879-5885, 1993
A;Title: Human gastric mucin. Identification of a unique species by expression cloning.
A;Reference number: A46629; MUID:93194895; PMID:7680650
A;Accession: B46629
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-505 <TOR>
A;Cross-references: UNIPROT:Q14395; UNIPARC:UPI0000070A7C; GB:L07518; NID:g292045; PIDN:
A;Experimental source: stomach
A;Note: sequence extracted from NCBI backbone (NCBIN:128397, NCBIP:128399)
C;Genetics:
A;Gene: GDB:MUC6
A;Cross-references: GDB:134734; OMIM:158374
A;Map position: 11p15.5-11p15.5
C;Keywords: glycoprotein

Query Match        6.5%;    Score 144.5;    DB 2;    Length 505;
Best Local Similarity  23.9%;    Pred. No. 0.031;
Matches   78;  Conservative   37;  Mismatches  101;  Indels  111;  Gaps  15;

Qy    89 TARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLH-GQPS 147
             :||:||  | |  |||:||||||||||||||:|  |::| | |:|::|:||:|| ||
Db   116 SSRPPPFTTHSPTGSSPFS-STGPMT--ATSFKT-TTTYPTSLPQTTPLTHVPPFS 170

Qy   148 QA-VTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQS 206
             || :|| || || :|  |:|
Db   171 TSLVTPITH---TVITPT-------------------------------------HPQ- 188

Qy   207 SQFSSDQEIAHLLPENVSALPATV----------------AVASPHTTSATPKPATLLP 249
             ||||:|:|| ::|||||:| |||                 :| ::||:||::|:|:::
Db   189 ---MSTSAYIHSTPTGTIASPTTVKATRSTYTAPLMTATTSRISQAHSSISTAKTSTSLH 245

Qy   250 TNAS--------------------VTPSGTSQPQLATTAPPVTVT----SQPPTTLIS--- 287
             |:||                    |||:|||||:|||||||||||    |||||||
Db   246 SHASSTHHPEVTPTSTTNVTPKSTSR---DTSTPVTHTTSATSSRPPPITTHSSPTRS 301

Qy   288 TRAAATLQAMATTAVLTTTFQAPTDSKGSLET-IPFTEISNLJLNTGNVYNPTALSMSNV 346
             |||||||||||||||:||||||||||||:|||  ||:|||::|:||:||||| |:::|||
Db   302 SPLSSTGPMTATSIKTTTTYPTPSHPQTLTTHVPPFSTSSVTPSTHTVITPTHAQMST- 360
```

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Qy    347 ESSTMNKTASWEGREASPGSSSQGSVP 373
              ||  |:  |:||
Db    361 -----------SASIHSTPTGTVP 373
```

Search completed: September 19, 2007, 18:43:22
Job time : 111 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2007, 18:42:23 ; Search time 342 Seconds
(without alignments)
1351.128 Million cell updates/sec

Title: US-10-677-471-83
Perfect score: 2211
Sequence: 1 MFFCGGEGSLTYTLVIICFLT.........LRRKRYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	2211	100.0	431	1	MANS1_HUMAN	Q9h8j5 homo sapien
2	2211	95.5	431	2	Q5RAU3_PONPY	Q5rau3 pongo pygma
3	2039	92.2	431	1	Q95KG7_MACFA	Q95kg7 macaca fasc
4	2022	91.5	397	2	Q9NW60_HUMAN	Q9nw60 homo sapien
5	1176.5	53.2	414	2	Q3TAH6_MOUSE	Q3tah6 mus musculu
6	1164.5	52.7	414	1	MANS1_MOUSE	Q9cr33 mus musculu
7	522	23.6	449	2	Q5ZKY8_CHICK	Q5zky8 gallus gall
8	503	22.7	194	2	Q8KOI0_MOUSE	Q8k0i0 mus musculu
9	197.5	8.9	392	2	Q8VCP2_MOUSE	Q8vcp2 mus musculu
10	197	8.9	449	2	Q9H2K4_HUMAN	Q9h2k4 homo sapien
11	196.5	8.9	392	2	Q9D8N1_MOUSE	Q9d8n1 m 10 day ol
12	188	8.5	449	2	Q96F05_HUMAN	Q96f05 homo sapien
13	180.5	8.2	1349	2	Q8WWQ4_HUMAN	Q8wwq4 homo sapien
14	168	7.6	519	2	Q7YTR7_CAEBL	Q7ytr7 caenorhabdi
15	165.5	7.5	477	2	Q4V7A5_RAT	Q4v7a5 rattus norv
16	163	7.4	4262	2	Q68SJ2_HUMAN	Q68sj2 homo sapien
17	163	7.4	4493	2	Q68SJ3_HUMAN	Q68sj3 homo sapien
18	160.5	7.3	477	2	Q14887_HUMAN	Q14887 homo sapien
19	159.5	7.2	576	2	Q61MD1_CAEBR	Q61md1 caenorhabdi
20	158	7.1	566	2	Q55SZ1_CRYNE	Q55sz1 cryptococcu
21	158	7.1	2691	2	Q16JD9_AEDAE	Q16jd9 aedes aegyp
22	157.5	7.1	2448	2	Q8WWO5_HUMAN	Q8wwo5 homo sapien
23	157	7.1	566	2	Q5KHC3_CRYNE	Q5khc3 cryptococcu
24	156.5	7.1	328	2	O00446_HUMAN	O00446 homo sapien
25	156.5	7.1	848	2	Q61G28_CAEBR	Q61g28 caenorhabdi
26	155.5	7.0	564	2	Q5CQC1_CRYPV	Q5cqc1 cryptospori
27	155.5	7.0	769	2	Q17921_CAEEL	Q17921 caenorhabdi
28	154.5	7.0	784	2	Q6CI85_YARLI	Q6ci85 yarrowia li
29	154	7.0	534	2	O94317_SCHPO	O94317 schizosacch
30	152.5	6.9	407	2	Q56459_CAEEL	Q56459 caenorhabdi
31	152	6.9	1473	2	Q54LY1_DICDI	Q54ly1 dictyosteli
32	151.5	6.9	1034	2	Q613E9_CAEBR	Q613e9 caenorhabdi
33	151.5	6.9	1317	1	YOU3_CAEEL	Q09550 caenorhabdi
34	150.5	6.8	382	2	Q9XZZ8_LJTSI	Q9xzz8 litomosoide
35	150.5	6.8	797	1	VGLX_EHV1B	P28968 equine herp
36	150.5	6.8	860	1	CHI2_COCIM	P54197 coccidioide
37	150.5	6.8	2482	2	Q61GF0_CAEBR	Q61gf0 caenorhabdi
38	149.5	6.8	5179	1	MUC2_HUMAN	Q02817 homo sapien
39	149.5	6.8	5703	1	MUC5B_HUMAN	Q9hc84 homo sapien
40	149	6.7	484	2	Q16KJ1_AEDAE	Q16kj1 aedes aegyp
41	149	6.7	943	1	YL61_SCHPO	Q8tfg9 schizosacch
42	148.5	6.7	791	1	Q66VC3_9ALPH	Q66vc3 equid herpe
43	148.5	6.7	1233	1	MUC5A_HUMAN	P98088 homo sapien
44	148	6.7	436	2	Q16KI5_AEDAE	Q16ki9 aedes aegyp
45	148	6.7	484	2	Q16KI8_AEDAE	Q16ki8 aedes aegyp
46	148	6.7	513	2	Q6V4A2_DROYA	Q6v4a2 drosophila
47	148	6.7	2299	2	Q6A564_9BACE	Q6a564 bacteroides
48	147.5	6.7	452	2	Q2FAU2_9BETA	Q2fau2 cercopithec
49	147.5	6.7	733	2	Q55E25_DICDI	Q55e25 dictyosteli
50	147.5	6.7	790	2	Q20599_CAEEL	Q20599 caenorhabdi
51	147.5	6.7	842	2	Q95QF5_CAEEL	Q95qf5 caenorhabdi
52	147.5	6.7	1609	1	FIG2_YEAST	P25653 saccharomyc
53	147	6.6	662	1	MUC1_XENLA	Q05049 xenopus lae
54	147	6.6	753	2	Q54SK9_DICDI	Q54sk9 dictyosteli
55	146.5	6.6	572	2	Q58SM0_DROME	Q58sm0 drosophila
56	146.5	6.6	572	2	Q58SM7_DROME	Q58sm7 drosophila
57	146.5	6.6	629	2	Q5ELT4_DROME	Q5elt4 drosophila
58	146.5	6.6	679	2	Q3UU21_MOUSE	Q3uu21 mus musculu
59	146	6.6	316	2	Q8V0M4_9ALPH	Q8v0m4 equid herpe
60	146	6.6	457	2	Q86AK1_DICDI	Q86ak1 dictyosteli
61	146	6.6	457	2	Q556T8_DICDI	Q556t8 dictyosteli
62	146	6.6	472	2	Q6BHG8_DEBHA	Q6bhg8 debaryomyce
63	145.5	6.6	184	2	Q7PRM2_ANOGA	Q7prm2 anopheles g
64	145.5	6.6	629	2	Q24017_DROME	Q24017 drosophila
65	145.5	6.6	629	2	Q5ELT0_DROME	Q5elt0 drosophila
66	145.5	6.6	629	2	Q5ELV0_DROME	Q5elv0 drosophila
67	145.5	6.6	716	2	Q9NYE4_HUMAN	Q9nye4 homo sapien
68	145.5	6.6	901	2	Q6CAJ2_YARLI	Q6caj2 yarrowia li
69	145	6.6	425	2	Q702W3_HHV1	Q702w3 human herpe
70	145	6.6	521	2	Q4P5G5_USTMA	Q4p5g5 ustilago ma
71	145	6.6	1079	2	Q9N4S7_CAEEL	Q9n4s7 caenorhabdi
72	144.5	6.5	377	1	MUC7_HUMAN	Q8tax7 homo sapien
73	144.5	6.5	505	2	Q14395_HUMAN	Q14395 homo sapien
74	144.5	6.5	629	2	Q5ELR9_DROME	Q5elr9 drosophila
75	144.5	6.5	629	2	Q5ELR5_DROME	Q5elr5 drosophila
76	144.5	6.5	629	2	Q5ELR7_DROME	Q5elr7 drosophila
77	144.5	6.5	741	2	Q54Q93_DICDI	Q54q93 dictyosteli
78	144.5	6.5	787	2	STUB_DROME	Q05319 drosophila
79	144.5	6.5	841	2	Q4Q5Z4_LEIMA	Q4q5z4 leishmania
80	144.5	6.5	928	2	Q4CQ84_TRYCR	Q4cq84 trypanosoma
81	144.5	6.5	1140	1	YM96_YEAST	Q04893 saccharomyc
82	144	6.5	630	2	Q5ELS1_DROME	Q5els1 drosophila
83	144	6.5	778	2	Q28DA4_XENTR	Q28da4 xenopus tro
84	144	6.5	1646	2	Q5CFZ6_CRYHO	Q5cfz6 cryptospori
85	144	6.5	22152	2	Q8WXI7_HUMAN	Q8wxi7 homo sapien
86	143.5	6.5	462	2	Q7PWE4_ANOGA	Q7pwe4 anopheles g
87	143.5	6.5	482	2	Q6BSZ9_DEBHA	Q6bsz9 debaryomyce
88	143.5	6.5	629	2	Q5ELS3_DROME	Q5els3 drosophila
89	143.5	6.5	908	2	Q59PF9_CANAL	Q59pf9 candida alb
90	143.5	6.5	1414	2	Q80Z22_MOUSE	Q80z22 mus musculu
91	143.5	6.5	2850	2	Q80T03_MOUSE	Q80t03 mus musculu
92	143.5	6.5	4588	2	Q4SQC2_TETNG	Q4sqc2 tetraodon n
93	143	6.5	334	2	Q6VAW0_ANOGA	Q6vaw0 anopheles g
94	143	6.5	575	2	Q58SM2_DROME	Q58sm2 drosophila
95	143	6.5	601	2	Q6V6S0_DROME	Q6v6s0 drosophila
96	143	6.5	626	1	PME17_MOUSE	060696 mus musculu
97	143	6.5	632	2	Q5ELT8_DROME	Q5elt8 drosophila
98	143	6.5	1258	2	Q4RGJ4_TETNG	Q4rgj4 tetraodon n
99	142.5	6.4	491	1	PME17_BOVIN	Q06154 bos taurus
100	142.5	6.4	629	2	Q5ELS7_DROME	Q5els7 drosophila
101	142.5	6.4	826	2	Q8V0L5_9ALPH	Q8v0l5 drosophila
102	142.5	6.4	866	1	VGLX_EHV1V	Q68w0 equine herp
103	142.5	6.4	866	1	O39781_9ALPH	O39781 equid herpe
104	142.5	6.4	867	2	O39782_9ALPH	O39782 equid herpe

#	Organism	ID Code		Length	Score	Value
105	Q9vtn2 drosophila	Q9VTN2_DROME	2	1514	6.4	142.5
106	SELPL_MOUSE	SELPL_MOUSE	1	397	6.4	142
107	Q9w4m2 drosophila	Q9W4M2_DROME	2	483	6.4	142
108	Q6v6s4 drosophila	Q6V6S4_DROME	2	601	6.4	142
109	Q6v6s2 drosophila	Q6V6S2_DROME	2	601	6.4	142
110	Q6cd44 yarrowia li	Q6CD44_YARLI	2	612	6.4	142
111	Q6un14 leishmania	Q6UN14_LEICH	2	627	6.4	142
112	Q9w468 drosophila	Q9W468_DROME	2	873	6.4	142
113	Q5elu4 drosophila	Q5ELU4_DROME	2	629	6.4	141.5
114	DAN4 YEAST	DAN4_YEAST	1	1161	6.4	141.5
115	Q72w07 brachydanio	Q72W07_BRARE	2	1391	6.4	141.5
116	Q4wip3 aspergillus	Q4WIP3_ASPFU	2	278	6.4	141
117	Q8vol6 equid herpe	Q8VOL6_9ALPH	2	374	6.4	141
118	Q76h84 streptococc	Q76H84_STRMU	2	538	6.4	141
119	Q9czb2 m 10, 11 da	Q9CZB2_MOUSE	2	626	6.4	141
120	Q54i94 dictyosteli	Q54I94_DICDI	2	1186	6.4	141
121	Q8jkf9 heliothis z	Q8JKF9_9VIRU	2	1505	6.4	141
122	Q22579 caenorhabdi	Q22579_CAEEL	2	1844	6.4	141
123	Q564z3 caenorhabdi	Q564Z3_CAEEL	2	245	6.4	140.5
124	Q4v3x0 drosophila	Q4V3X0_DROME	2	294	6.4	140.5
125	Q9xwn5 caenorhabdi	Q9XWN5_CAEEL	2	370	6.4	140.5
126	Q8vom0 equid herpe	Q8VOM0_9ALPH	2	389	6.4	140.5
127	Q4v3z8 drosophila	Q4V3Z8_DROME	2	488	6.4	140.5
128	O43418 homo sapien	O43418_HUMAN	2	513	6.4	140.5
129	Q58sm6 drosophila	Q58SM6_DROME	2	572	6.4	140.5
130	Q58sm4 drosophila	Q58SM4_DROME	2	572	6.4	140.5
131	Q9v3h7 drosophila	Q9V3H7_DROME	2	629	6.4	140.5
132	Q5els8 drosophila	Q5ELS8_DROME	2	629	6.4	140.5
133	P87107 saccharomyc	P87107_YEAST	2	849	6.4	140.5
134	Q1ear5 coccidioide	Q1EAR5_COCIM	2	870	6.4	140.5
135	Q6cru1 kluyveromyc	Q6CRU1_KLULA	2	1423	6.4	140.5
136	Q8vol9 equid herpe	Q8VOL9_9ALPH	2	332	6.3	140
137	Q7tfv2 rhesus cyto	Q7TFV2_RHCM6	2	461	6.3	140
138	O76602 caenorhabdi	O76602_CAEEL	2	1275	6.3	140
139	Q967d0 geodia cydo	Q967D0_GEOCY	2	538	6.3	139.5
140	Q5elv3 drosophila	Q5ELV3_DROYA	2	669	6.3	139.5
141	Q30013 streptococc	Q30013_STRSU	2	1237	6.3	139.5
142	Q2fdk5 staphylococ	Q2FDK5_STAA3	2	2271	6.3	139.5
143	Q6vav9 anopheles g	Q6VAV9_ANOGA	2	334	6.2	139
144	Q8vol8 equid herpe	Q8VOL8_9ALPH	2	342	6.2	139
145	Q8vom3 equid herpe	Q8VOM3_9ALPH	2	372	6.2	139
146	O76810 anopheles g	O76810_ANOGA	2	373	6.2	139
147	Q5b4u2 emericella	Q5B4U2_EMENI	2	565	6.2	139
148	Q4qgj2 leishmania	Q4QGJ2_LEIMA	2	648	6.2	139
149	Q9vt17 drosophila	Q9VT17_DROME	2	1937	6.2	139
150	Q4rfa1 tetraodon n	Q4RFA1_TETNG	2	541	6.2	138.5
151	Q4qgk4 leishmania	Q4QGK4_LEIMA	2	668	6.2	138.5
152	Q29qw1 drosophila	Q29QW1_DROME	2	1108	6.2	138.5
153	Q9vu22 drosophila	Q9VU22_DROME	2	1371	6.2	138.5
154	Q8iq18 drosophila	Q8IQ18_DROME	2	23015	6.2	138.5
155	Q6vav6 anopheles g	Q6VAV6_ANOGA	2	334	6.2	138
156	Q8vom1 equid herpe	Q8VOM1_9ALPH	2	337	6.2	138
157	Q5a219 candida alb	Q5A219_CANAL	2	369	6.2	138
158	Q8cjd9 rattus norv	Q8CJD9_RAT	2	573	6.2	138
159	Q54px8 dictyosteli	Q54PX8_DICDI	2	676	6.2	138
160	Q2t9h8 xenopus lae	Q2T9H8_XENLA	2	815	6.2	138
161	Q86b02 dictyosteli	Q86B02_DICDI	2	2454	6.2	138
162	Q550k8 dictyosteli	Q550K8_DICDI	2	2454	6.2	138
163	Q8vol7 equid herpe	Q8VOL7_9ALPH	2	356	6.2	137.5
164	Q8vom2 equid herpe	Q8VOM2_9ALPH	2	357	6.2	137.5
165	Q58sm1 drosophila	Q58SM1_DROME	2	572	6.2	137.5
166	Q5els5 drosophila	Q5ELS5_DROME	2	629	6.2	137.5
167	Q5b9b7 emericella	Q5B9B7_EMENI	2	652	6.2	137.5
168	Q4qgk1 leishmania	Q4QGK1_LEIMA	2	704	6.2	137.5
169	Q6r8j4 brachydanio	Q6R8J4_BRARE	2	841	6.2	137.5
170	Q6r8j3 brachydanio	Q6R8J3_BRARE	2	935	6.2	137.5
171	Q6r8j2 brachydanio	Q6R8J2_BRARE	2	977	6.2	137.5
172	Q54s26 dictyosteli	Q54S26_DICDI	2	1117	6.2	137.5
173	Q63661 rattus norv	Q63661_RAT	2	1805	6.2	137.5
174	Q6g620 staphylococ	Q6G620_STAAS	2	2275	6.2	137.5
175	Q8nuj3 staphylococ	Q8NUJ3_STAAW	2	2275	6.2	137.5
176	Q17e94 aedes aegyp	Q17E94_AEDAE	2	2308	6.2	137.5
177	Q8uzf3 cercopithec	Q8UZF3_9GAMA	2	259	6.2	137
178	Q6vav4 anopheles g	Q6VAV4_ANOGA	2	334	6.2	137
179	Q62170 mus musculu	Q9C247_NEUCR	2	464	6.2	137
180	Q9w4m2 drosophila	Q58SN2_DROME	2	519	6.2	137
181	Q6v6s4 drosophila	Q58SN1_DROME	2	519	6.2	137
182	Q6v6s2 drosophila	Q58SN3_DROME	2	522	6.2	137
183	Q6cd44 yarrowia li	Q58SM8_DROME	2	522	6.2	137
184	Q6un14 leishmania	Q58SN0_DROME	2	522	6.2	137
185	Q9w468 drosophila	Q29071_PIG	2	528	6.2	137
186	Q5elu4 drosophila	Q8MT56_DROME	2	579	6.2	137
187	Q9vb46 drosophila	Q9VB46_DROME	2	579	6.2	137
188	Q5tt09 anopheles g	Q5TT09_ANOGA	2	812	6.2	137
189	Q6c461 yarrowia li	Q6C461_YARLI	2	890	6.2	137
190	Q8ir52 drosophila	Q8IR52_DROME	2	3269	6.2	137
191	Q8jzm8 mus musculu	Q8JZM8_MOUSE	2	3443	6.2	137
192	Q58sm3 drosophila	Q58SM3_DROME	2	574	6.2	136.5
193	Q5elp3 drosophila	Q5ELP3_DROSI	2	624	6.2	136.5
194	Q8mp19 dictyosteli	Q8MP19_DICDI	2	627	6.2	136.5
195	Q555l9 dictyosteli	Q555L9_DICDI	2	681	6.2	136.5
196	Q1u210 mycobacteri	Q1U210_9MYCO	2	844	6.2	136.5
197	Q1tn86 mycobacteri	Q1TN86_9MYCO	2	847	6.2	136.5
198	Q1b8j9 mycobacteri	Q1B8J9_9MYCO	2	847	6.2	136.5
199	Q55bs4 dictyosteli	Q55BS4_DICDI	2	966	6.2	136.5
200	Q94185 caenorhabdi	Q94185_CAEEL	2	1254	6.2	136.5
201	Q4pov7 ustilago ma	Q4POV7_USTMA	2	1259	6.2	136.5
202	Q3u0f1 mus musculu	Q3U0F1_MOUSE	2	417	6.2	136
203	Q61au9 caenorhabdi	Q61AU9_CAEBR	2	479	6.2	136
204	P53832 saccharomyc	WSC2_YEAST	1	503	6.2	136
205	Q9vn36 drosophila	Q9VN36_DROME	2	559	6.2	136
206	Q24160 drosophila	Q24160_DROME	2	582	6.2	136
207	Q6v6s1 drosophila	Q6V6S1_DROME	2	601	6.2	136
208	P98168 homo sapien	ZXDA_HUMAN	1	799	6.2	136
209	Q5hcp3 staphylococ	Q5HCP3_STAAC	2	2261	6.2	135.5
210	Q09624 caenorhabdi	YS89_CAEEL	1	3178	6.2	135.5
211	Q62605 rattus norv	Q62605_RAT	2	322	6.1	135.5
212	Q6ctm5 kluyveromyc	Q6CTM5_KLULA	2	520	6.1	135.5
213	Q14879 homo sapien	Q14879_HUMAN	2	543	6.1	135.5
214	Q5eln9 drosophila	Q5ELN9_DROSI	2	624	6.1	135.5
215	Q5elp7 drosophila	Q5ELP7_DROSI	2	625	6.1	135.5
216	Q4p867 ustilago ma	Q4P867_USTMA	2	836	6.1	135.5
217	Q1zx99 dictyosteli	Q1ZX99_DICDI	2	1024	6.1	135.5
218	Q555d2 dictyosteli	Q555D2_DICDI	2	1061	6.1	135.5
219	Q5t197 homo sapien	Q5T197_HUMAN	2	1183	6.1	135.5
220	Q9nsm8 homo sapien	Q9NSM8_HUMAN	2	1299	6.1	135.5
221	Q869r4 dictyosteli	Q869R4_DICDI	2	1806	6.1	135.5
222	Q1ycs7 staphylococ	Q1YCS7_STAAU	2	2271	6.1	135.5
223	Q1y565 staphylococ	Q1Y565_STAAU	2	2271	6.1	135.5
224	Q99qy4 staphylococ	Q99QY4_STAAM	2	2271	6.1	135.5
225	Q7a362 staphylococ	Q7A362_STAAN	2	2271	6.1	135.5
226	Q54qc0 dictyosteli	Q54QC0_DICDI	2	2381	6.1	135.5
227	Q9y520 homo sapien	Q9Y520_HUMAN	2	2701	6.1	135.5
228	Q5t199 homo sapien	Q5T199_HUMAN	2	2703	6.1	135.5
229	Q9hdv8 schizosacch	Q9HDV8_SCHPO	2	244	6.1	135
230	Q5tpb1 anopheles g	Q5TPB1_ANOGA	2	321	6.1	135
231	Q6vav5 anopheles g	Q6VAV5_ANOGA	2	334	6.1	135
232	Q5i5k5 meleagris g	Q5I5K5_MELGA	2	403	6.1	135
233	Q3dve9 chloroflexu	Q3DVE9_CHLAU	2	432	6.1	135
234	Q4ich3 gibberella	Q4ICH3_GIBZE	2	500	6.1	135
235	Q5elu2 drosophila	Q5ELU2_DROME	2	632	6.1	135
236	P98169 homo sapien	ZXDB_HUMAN	1	803	6.1	135
237	Q4cpm9 trypanosoma	Q4CPM9_TRYCR	2	1077	6.1	135
238	Q63549 rattus norv	Q63549_RAT	2	309	6.1	134.5
239	Q5apq2 candida alb	Q5APQ2_CANAL	2	768	6.1	134.5
240	Q4w973 aspergillus	Q4W973_ASPFU	2	970	6.1	134.5
241	O76894 drosophila	O76894_DROME	2	1795	6.1	134.5
242	Q14851 homo sapien	Q14851_HUMAN	2	164	6.1	134
243	Q4qgl0 leishmania	Q4QGL0_LEIMA	2	303	6.1	134
244	Q5elu8 drosophila	Q5ELU8_DROME	2	632	6.1	134
245	Q5elu0 drosophila	Q5ELU0_DROME	2	632	6.1	134
246	O35930 mus musculu	O35930_MOUSE	2	734	6.1	134
247	Q5sx47 mus musculu	Q5SX47_MOUSE	2	734	6.1	134
248	Q5b819 emericella	Q5B819_EMENI	2	828	6.1	134
249	Q871y4 neurospora	Q871Y4_NEUCR	2	1642	6.1	134
250	Q869l1 dictyosteli	Q869L1_DICDI	2	2053	6.1	134

No.	Sc1	Sc2	pI	Len	n	SeqID	Accession	Species
251	134	133.5	6.1	2109	2	Q552X2_DICDI	Q552x2	dictyosteli
252	133.5	133	6.0	333	2	Q6VAV8_ANOGA	Q6vav8	anopheles g
253	133.5	133	6.0	347	2	Q658M7_HUMAN	Q658m7	homo sapien
254	133.5	133	6.0	375	2	Q55F61_DICDI	Q55f61	dictyosteli
255	133.5	133	6.0	624	2	Q58SG1_DROSI	Q58sg1	drosophila
256	133.5	133	6.0	624	2	Q58SF9_DROSI	Q58sf9	drosophila
257	133.5	133	6.0	677	2	Q28256_CANFA	Q28256	canis famil
258	133.5	133	6.0	708	2	Q18175_CAEBR	Q18175	caenorhabdi
259	133.5	133	6.0	1014	2	Q25C37_9SACH	Q25c37	pichia minu
260	133	132.5	6.0	1984	2	Q400N0_DROME	Q400n0	drosophila
261	133	132.5	6.0	274	2	Q1XBT2_BHV4	Q1xbt2	bovine herp
262	133	132.5	6.0	398	2	Q8C265_MOUSE	Q8c265	mus musculu
263	133	132.5	6.0	417	2	Q3TA56_MOUSE	Q3ta56	mus musculu
264	133	132.5	6.0	515	2	Q2PFT9_MACFA	Q2pft9	macaca fasc
265	133	132.5	6.0	556	1	WSC3_YEAST	WSC3	saccharomyc
266	133	132.5	6.0	636	1	YNR6_YEAST	YNR6	saccharomyc
267	133	132.5	6.0	876	2	Q61915_CAEBR	Q61915	caenorhabdi
268	133	132.5	6.0	970	2	Q54MI9_DICDI	Q54mi9	dictyosteli
269	133	132.5	6.0	971	2	Q6W3C4_CAEEL	Q6w3c4	caenorhabdi
270	133	132.5	6.0	989	2	Q19930_CAEBR	Q19930	caenorhabdi
271	133	132.5	6.0	1051	2	Q6C1J9_YARLI	Q6c1j9	yarrowia li
272	133	132.5	6.0	1075	1	FLO5_YEAST	FLO5	saccharomyc
273	132.5	132	6.0	1132	2	Q7RAI4_PLAYO	Q7rai4	plasmodium
274	132.5	132	6.0	1304	2	Q4N342_THEPA	Q4n342	theileria p
275	132.5	132	6.0	413	2	Q5B569_EMENI	Q5b569	emericella
276	132.5	132	6.0	434	2	Q872V2_NEUCR	Q872v2	neurospora
277	132.5	132	6.0	500	2	Q58SI6_DROSI	Q58si6	drosophila
278	132.5	132	6.0	624	2	Q58SF4_DROSI	Q58sf4	drosophila
279	132.5	132	6.0	624	2	Q5ELN5_DROSI	Q5eln5	drosophila
280	132	131.5	6.0	698	2	Q61SH2_CAEBR	Q61sh2	caenorhabdi
281	132	131.5	6.0	1175	2	Q9VRL7_DROME	Q9vrl7	drosophila
282	132	131.5	6.0	1293	2	Q17GE7_AEDAE	Q17ge7	aedes aegyp
283	132	131.5	6.0	2271	2	Q2FUW1_STAA8	Q2fuw1	staphylococ
284	132	131.5	6.0	298	2	Q6CNP4_KLULA	Q6cnp4	kluyveromyc
285	132	131.5	6.0	452	2	Q4CL35_TRYCR	Q4cl35	trypanosoma
286	132	131.5	6.0	452	2	Q17CX1_AEDAE	Q17cx1	aedes aegyp
287	132	131.5	6.0	522	2	Q58SN4_DROME	Q58sn4	drosophila
288	132	131.5	6.0	622	2	Q58SH9_DROSI	Q58sh9	drosophila
289	132	131.5	6.0	622	2	Q5ELQ5_DROSI	Q5elq5	drosophila
290	132	131.5	6.0	622	2	Q6VEE2_DROSI	Q6vee2	drosophila
291	132	131.5	6.0	622	2	Q58SF6_DROSI	Q58sf6	drosophila
292	132	131.5	6.0	622	2	Q58SG2_DROSI	Q58sg2	drosophila
293	132	131.5	6.0	622	2	Q6VEE4_DROSI	Q6vee4	drosophila
294	132	131.5	6.0	622	2	Q6V6D8_DROSI	Q6v6d8	drosophila
295	132	131.5	6.0	625	2	Q5ELQ9_DROSI	Q5elq9	drosophila
296	132	131.5	6.0	625	2	Q58SF8_DROSI	Q58sf8	drosophila
297	132	131.5	6.0	625	2	Q5ELP1_DROSI	Q5elp1	drosophila
298	132	131.5	6.0	788	2	Q58SH7_DROSI	Q58sh7	drosophila
299	131.5	131	6.0	807	2	O18510_TRINI	O18510	trichoplusi
300	131.5	131	6.0	1162	2	O18511_TRINI	O18511	trichoplusi
301	131.5	131	6.0	1236	1	TCNA_TRYCR	P23253	trypanosoma
302	131.5	131	6.0	1316	2	Q9C105_SCHPO	Q9c105	schizosacch
303	131.5	131	6.0	1589	2	Q1ZXH8_DICDI	Q1zxh8	dictyosteli
304	131.5	131	6.0	348	2	Q54I34_DICDI	Q54i34	dictyosteli
305	131.5	131	6.0	389	2	Q61TG5_CAEBR	Q61tg5	caenorhabdi
306	131.5	131	5.9	497	2	Q61IZ9_CAEBR	Q61iz9	caenorhabdi
307	131.5	131	5.9	582	2	Q58SI7_DROSI	Q58si7	drosophila
308	131	130.5	5.9	624	2	Q8IR74_DROME	Q8ir74	drosophila
309	131	130.5	5.9	760	2	Q58SF2_DROSI	Q58sf2	drosophila
310	131	130.5	5.9	725	2	Q4QGI8_LEIMA	Q4qgi8	leishmania
311	131	130.5	5.9	2163	2	Q61TS1_CAEBR	Q61ts1	caenorhabdi
312	131	130.5	5.9	5317	2	Q8TA74_HEMPU	Q8ta74	hemicentrot
313	131	130.5	5.9	378	2	Q7QFG1_ANOGA	Q7qfg1	anopheles g
314	131	130.5	5.9	397	2	Q99J34_MOUSE	Q99j34	mus musculu
315	131	130.5	5.9	469	2	Q7J48_CERAE	Q7j48	cercopithec
316	131	130.5	5.9	474	2	O46597_CERAE	O46597	cercopithec
317	131	130.5	5.9	494	2	Q58SI3_DROSI	Q58si3	drosophila
318	131	130.5	5.9	642	2	Q75JG6_DICDI	Q75jg6	dictyosteli
319	131	130.5	5.9	681	2	Q552J1_DICDI	Q552j1	dictyosteli
320	131	130.5	5.9	725	1	AGA1_YEAST	AGA1	saccharomyc
321	131	130.5	5.9	738	2	Q5WN81_CAEBR	Q5wn81	caenorhabdi
322	131	130.5	5.9	823	2	Q54Y28_DICDI	Q54y28	dictyosteli
323	131	130.5	5.9	1376	2	Q4N457_THEPA	Q4n457	theileria p
324	131	130.5	5.9	1521	2	Q7Q1W8_ANOGA	Q7q1w8	anopheles g
325	130.5	130	5.9	234	2	Q1HVD8_EBVG	Q1hvd8	epstein-bar
326	130.5	130	5.9	354	2	Q2U8L4_ASPOR	Q2u8l4	aspergillus
327	130.5	130	5.9	519	2	Q58SM9_DROME	Q58sm9	drosophila
328	130.5	130	5.9	524	1	P60_LISIV	O01837	listeria iv
329	130.5	130	5.9	624	2	Q5ELN1_DROSI	Q5eln1	drosophila
330	130.5	130	5.9	625	2	Q58SF7_DROSI	Q58sf7	drosophila
331	130.5	130	5.9	708	2	Q73H41_WOLPM	Q73h41	wolbachia p
332	130	129.5	5.9	847	2	Q6FKG2_CANGA	Q6fkg2	candida gla
333	130	129.5	5.9	912	2	Q5B926_EMENI	Q5b926	emericella
334	130	129.5	5.9	494	2	Q58SI4_DROSI	Q58si4	drosophila
335	130	129.5	5.9	495	2	Q58SK3_DROSI	Q58sk3	drosophila
336	130	129.5	5.9	510	2	Q6SCJ8_ASPFU	Q6scj8	aspergillus
337	130	129.5	5.9	547	1	MUC13_RAT	P97881	rattus norv
338	130	129.5	5.9	547	2	Q5AP56_CANAL	Q5ap56	candida alb
339	130	129.5	5.9	572	2	Q4QGJ6_LEIMA	Q4qgj6	leishmania
340	130	129.5	5.9	593	2	Q7S8P1_NEUCR	Q7s8p1	neurospora
341	130	129.5	5.9	625	2	Q6V6E1_DROSI	Q6v6e1	drosophila
342	130	129.5	5.9	625	2	Q58SH8_DROSI	Q58sh8	drosophila
343	130	129.5	5.9	625	2	Q5ELN3_DROSI	Q5eln3	drosophila
344	130	129.5	5.9	625	2	Q58SF3_DROSI	Q58sf3	drosophila
345	129.5	129	5.9	817	2	Q54YV1_DICDI	Q54yv1	dictyosteli
346	129.5	129	5.9	824	2	Q6H8T3_SPAJD	Q6h8t3	spalax juda
347	129.5	129	5.9	1241	2	Q75JC0_DICDI	Q75jc0	dictyosteli
348	129.5	129	5.9	1241	2	Q55AM6_DICDI	Q55am6	dictyosteli
349	129.5	129	5.9	333	2	Q6VAV7_ANOGA	Q6vav7	anopheles g
350	129.5	129	5.9	400	1	MUA1_XENLA	P10667	xenopus lae
351	129.5	129	5.9	482	2	Q5TG0_CRYNE	Q5tg0	cryptococcu
352	129.5	129	5.9	482	2	Q5KIX7_CRYNE	Q5kix7	cryptococcu
353	129.5	129	5.9	552	2	Q4N6B9_THEPA	Q4n6b9	theileria p
354	129.5	129	5.9	651	2	Q61YZ5_CAEBR	Q61yz5	caenorhabdi
355	129.5	129	5.9	825	2	Q7YZW4_CAEEL	Q7yzw4	caenorhabdi
356	129.5	129	5.9	927	2	Q4HXL6_GIBZE	Q4hxl6	gibberella
357	129.5	129	5.9	1032	2	P91365_CAEEL	P91365	caenorhabdi
358	129	128.5	5.9	1103	2	Q2GKG3_ANAPZ	Q2gkg3	anaplasma p
359	129	128.5	5.9	1115	2	Q7RPL1_PLAYO	Q7rpl1	plasmodium
360	129	128.5	5.9	1367	1	MUC1_YEAST	P08640	saccharomyc
361	129	128.5	5.8	1367	2	Q6LCS8_SACDI	Q61cs8	saccharomyc
362	129	128.5	5.8	1708	2	Q1F1X0_9CHLR	Q1f1x0	roseiflexus
363	129	128.5	5.8	1752	2	Q9AE52_RUMFL	Q9ae52	ruminococcu
364	129	128.5	5.8	2232	2	Q8IFX6_CAEEL	Q8ifx6	caenorhabdi
365	129	128.5	5.8	4377	1	HUWE1_MOUSE	Q7tmy8	mus musculu
366	129	128.5	5.8	4378	2	Q4JG03_MOUSE	Q4jg03	mus musculu
367	129	128.5	5.8	197	2	Q26878_TRYCR	Q26878	trypanosoma
368	129	128.5	5.8	279	2	Q14888_HUMAN	Q14888	homo sapien
369	129	128.5	5.8	318	2	Q16MH7_AEDAE	Q16mh7	aedes aegyp
370	129	128.5	5.8	411	2	Q2UG37_ASPOR	Q2ug37	aspergillus
371	129	128.5	5.8	473	2	Q7J47_CERAE	Q7j47	cercopithec
372	129	128.5	5.8	478	2	O46598_CERAE	O46598	cercopithec
373	128.5	128	5.8	495	2	Q58SI5_DROSI	Q58sj5	drosophila
374	128.5	128	5.8	739	2	O02360_CAEEL	O02360	caenorhabdi
375	128.5	128	5.8	1196	2	Q5H935_HUMAN	Q5h935	homo sapien
376	128.5	128	5.8	1199	2	Q5CEX1_CRYHO	Q5cex1	cryptospori
377	128.5	128	5.8	1325	2	Q75JA1_DICDI	Q75ja1	dictyosteli
378	128.5	128	5.8	1325	2	Q55AK3_DICDI	Q55ak3	dictyosteli
379	128.5	128	5.8	1483	2	Q7KWU3_DICDI	Q7kwu3	dictyosteli
380	128.5	128	5.8	1493	2	Q55917_DICDI	Q55917	dictyosteli
381	128.5	128	5.8	1562	2	Q3MP25_CANAL	Q3mp25	candida alb
382	128.5	128	5.8	1937	2	Q5CY21_CRYPV	Q5cy21	cryptospori
383	128.5	128	5.8	2039	2	Q54F78_DICDI	Q54f78	dictyosteli
384	128.5	128	5.8	3407	2	Q5H924_HUMAN	Q5h924	homo sapien
385	128.5	128	5.8	4374	1	HUWE1_HUMAN	Q7z6z7	homo sapien
386	128.5	128	5.8	234	1	VGP8_EBV	P03224	epstein-bar
387	128.5	128	5.8	234	2	Q777C5_EBVG	Q777c5	epstein-bar
388	128.5	128	5.8	424	2	Q2U7S7_ASPOR	Q2u7s7	aspergillus
389	128.5	128	5.8	486	2	Q17H66_AEDAE	Q17h66	aedes aegyp
390	128.5	128	5.8	585	2	Q58SG4_DROSI	Q58sg4	drosophila
391	128.5	128	5.8	634	2	Q59TL7_CANAL	Q59tl7	candida alb
392	128.5	128	5.8	856	2	O56854_EBVG	O56854	epstein-bar
393	128.5	128	5.8	981	2	Q54SW0_DICDI	Q54sw0	dictyosteli
394	128.5	128	5.8	1720	2	Q8I486_PLAF7	Q8i486	plasmodium
395	128.5	128	5.8	11696	2	Q5CV09_CRYPV	Q5cv09	cryptospori
396	128	127.5	5.8	244	2	Q5TTY6_ANOGA	Q5tty6	anopheles g

No.	Score	pI	Length	Entry	N	Accession	Organism
397	128	5.8	318	Q17LU9_AEDAE	2	Q17lu9	aedes aegyp
398	128	5.8	490	Q6V6N2_DROSI	2	Q6v6n2	drosophila
399	128	5.8	490	Q6V6N4_DROSI	2	Q6v6n4	drosophila
400	128	5.8	490	Q6V6N6_DROSI	2	Q6v6n6	drosophila
401	128	5.8	492	Q58SJ6_DROSI	2	Q58sj6	drosophila
402	128	5.8	493	Q58SJ0_DROSI	2	Q58sj0	drosophila
403	128	5.8	494	Q58SJ4_DROSI	2	Q58sj4	drosophila
404	128	5.8	494	Q58SK0_DROSI	2	Q58sk0	drosophila
405	128	5.8	494	Q58SI1_DROSI	2	Q58si1	drosophila
406	128	5.8	495	Q58SK1_DROSI	2	Q58sk1	drosophila
407	128	5.8	495	Q58SK4_DROSI	2	Q58sk4	drosophila
408	128	5.8	495	Q58SJ3_DROSI	2	Q58sj3	drosophila
409	128	5.8	495	Q58SJ1_DROSI	2	Q58sj1	drosophila
410	128	5.8	495	Q58SI8_DROSI	2	Q58si8	drosophila
411	128	5.8	495	Q58SK6_DROSI	2	Q58sk6	drosophila
412	128	5.8	495	Q58SK7_DROSI	2	Q58sk7	drosophila
413	128	5.8	495	Q58SJ2_DROSI	2	Q58sj2	drosophila
414	128	5.8	495	Q58SL0_DROSI	2	Q58sl0	drosophila
415	128	5.8	495	Q58SJ5_DROSI	2	Q58sj5	drosophila
416	128	5.8	495	Q58SI2_DROSI	2	Q58si2	drosophila
417	128	5.8	495	Q58SK2_DROSI	2	Q58sk2	drosophila
418	128	5.8	510	CX56_CHICK	1	P29415	gallus gall
419	128	5.8	605	WSC4_YEAST	1	P38739	saccharomyc
420	128	5.8	624	Q4S289_TETNG	1	Q4s289	tetraodon n
421	128	5.8	693	Q27394_CAEEL	2	Q27394	caenorhabdi
422	128	5.8	709	O16783_CAEEL	2	O16783	caenorhabdi
423	128	5.8	795	Q6CSM1_KLULA	2	Q6csm1	kluyveromyc
424	128	5.8	870	SYP1_YEAST	1	P25623	saccharomyc
425	128	5.8	881	Q8IMS9_DROME	2	Q8ims9	drosophila
426	128	5.8	1092	Q9UVY2_PNECA	2	Q9uvy2	pneumocysti
427	128	5.8	1143	Q17J23_AEDAE	2	Q17j23	aedes aegyp
428	128	5.8	1153	Q80TK3_MOUSE	2	Q80tk3	mus musculu
429	128	5.8	1256	Q675X6_OIKDI	2	Q675x6	oikopleura
430	128	5.8	1773	Q4N437_THEPA	2	Q4n437	theileria p
431	128	5.8	1816	Q4N6E9_THEPA	2	Q4n6e9	theileria p
432	127.5	5.8	234	Q3KSQ8_EBVG	2	Q3ksq8	epstein-bar
433	127.5	5.7	297	Q7PR65_ANOGA	2	Q7pr65	anopheles g
434	127.5	5.7	466	Q55IY7_CRYNE	1	Q55iy7	cryptococcu
435	127.5	5.7	523	Q84DU4_LISIV	2	Q84du4	listeria iv
436	127.5	5.7	526	Q16LH4_AEDAE	2	Q16lh4	aedes aegyp
437	127.5	5.7	540	EGR1_BOVIN	1	Q29w20	bos taurus
438	127.5	5.7	559	CAF1B_HUMAN	1	Q13112	homo sapien
439	127.5	5.7	567	Q4P6Q2_USTMA	2	Q4p6q2	ustilago ma
440	127.5	5.7	577	Q8N8I1_HUMAN	2	Q8n8i1	homo sapien
441	127.5	5.7	582	Q58SG6_DROSI	2	Q58sg6	drosophila
442	127.5	5.7	629	Q6MW02_NEUCR	2	Q6mw02	neurospora
443	127.5	5.7	634	HWP1_CANAL	1	P46593	candida alb
444	127.5	5.7	687	Q3E273_CHLAU	2	Q3e273	chloroflexu
445	127.5	5.7	915	Q54BC9_DICDI	2	Q54bc9	dictyosteli
446	127.5	5.7	970	Q54IY4_DICDI	2	Q54iy4	dictyosteli
447	127.5	5.7	980	Q5TPB2_ANOGA	2	Q5tpb2	anopheles g
448	127.5	5.7	1135	Q6BXC0_DEBHA	2	Q6bxc0	debaryomyce
449	127.5	5.7	1677	Q8I127_CAEEL	2	Q8i127	caenorhabdi
450	127.5	5.7	1838	Q18657_CAEEL	2	Q18657	caenorhabdi
451	127.5	5.7	1878	Q6CP24_KLULA	2	Q6cp24	kluyveromyc
452	127	5.7	377	Q16P49_AEDAE	2	Q16p49	aedes aegyp
453	127	5.7	421	O15329_HUMAN	2	O15329	homo sapien
454	127	5.7	495	Q58SJ7_DROSI	2	Q58sj7	drosophila
455	127	5.7	495	Q58SK8_DROSI	2	Q58sk8	drosophila
456	127	5.7	500	Q3TNW5_MOUSE	2	Q3tnw5	m 0 day neo
457	126.5	5.7	852	Q6XP42_9CLOT	2	Q6xp42	acetivibrio
458	126.5	5.7	1322	FLO9_YEAST	1	P39712	saccharomyc
459	126.5	5.7	1472	Q6V9R4_STRPU	2	Q6v9r4	strongyloce
460	126.5	5.7	1550	Q54GS1_DICDI	2	Q54gs1	dictyosteli
461	126.5	5.7	1657	Q76NT8_DICDI	2	Q76nt8	dictyosteli
462	126.5	5.7	1657	Q542N0_DICDI	2	Q542n0	dictyosteli
463	126.5	5.7	314	Q88TS7_LACPL	2	Q88ts7	lactobacill
464	126.5	5.7	327	Q25334_LEIMA	2	Q25334	leishmania
465	126.5	5.7	354	Q25402_LIITSI	2	Q25402	litomosoide
466	126.5	5.7	371	Q25333_LEIMA	2	Q25333	leishmania
467	126.5	5.7	466	Q5KCR4_CRYNE	2	Q5kcr4	cryptococcu
468	126.5	5.7	467	Q6C5E7_YARLI	2	Q6c5e7	yarrowia li
469	126.5	5.7	507	Q5CF50_CRYHO	2	Q5cf50	cryptospori
470	126.5	5.7	596	Q16G62_AEDAE	2	Q16g62	aedes aegyp
471	126.5	5.7	624	Q58SF5_DROSI	2	Q58sf5	drosophila
472	126.5	5.7	648	Q95QX0_CAEEL	2	Q95qx0	caenorhabdi
473	126.5	5.7	709	Q86IX4_DICDI	2	Q86ix4	dictyosteli
474	126.5	5.7	709	Q55SZ9_DICDI	2	Q55sz9	dictyosteli
475	126.5	5.7	716	Q4P695_USTMA	2	Q4p695	ustilago ma
476	126.5	5.7	800	Q8TFG4_SCHPO	2	Q8tfg4	schizosacch
477	126.5	5.7	858	Q9C470_CANAL	2	Q9c470	candida alb
478	126.5	5.7	1029	Q8TDH7_HUMAN	2	Q8tdh7	homo sapien
479	126.5	5.7	1140	Q8SSN9_DICDI	2	Q8ssn9	dictyosteli
480	126.5	5.7	1140	Q55SL0_DICDI	2	Q55sl0	dictyosteli
481	126.5	5.7	1260	ALS1_CANAL	1	P46590	candida alb
482	126.5	5.7	1260	Q5A8L0_CANAL	2	Q5a8l0	candida alb
483	126.5	5.7	1260	Q5A8T4_CANAL	2	Q5a8t4	candida alb
484	126.5	5.7	1832	O96503_CRYPV	2	O96503	cryptospori
485	126.5	5.7	2175	O45881_CAEEL	2	O45881	caenorhabdi
486	126.5	5.7	2338	Q759S3_ASHGO	2	Q759s3	ashbya goss
487	126.5	5.7	2799	GP112_HUMAN	1	Q8izf6	homo sapien
488	126.5	5.7	2804	Q5UVK3_HUMAN	2	Q5ivk3	homo sapien
489	126.5	5.7	337	Q3UU94_MOUSE	2	Q3uu94	mus musculu
490	126	5.7	405	SDC3_CHICK	1	P26261	gallus gall
491	126	5.7	405	Q4WNK1_ASPFU	1	Q4wnk1	aspergillus
492	126	5.7	483	LRP11_MOUSE	1	Q8cb67	mus musculu
493	126	5.7	542	Q17QJ4_BOVIN	1	Q17qj4	bos taurus
494	126	5.7	625	Q58SG0_DROSI	2	Q58sg0	drosophila
495	126	5.7	636	Q4LE84_PIG	1	Q4le84	sus scrofa
496	126	5.7	659	Q86AI8_DICDI	2	Q86ai8	dictyosteli
497	126	5.7	659	Q556Y6_DICDI	2	Q556y6	dictyosteli
498	126	5.7	703	Q16TC8_AEDAE	2	Q16tc8	aedes aegyp
499	126	5.7	777	Q9VXA5_DROME	2	Q9vxa5	drosophila
500	126	5.7	822	Q7KUX2_DROME	2	Q7kux2	drosophila
501	126	5.7	908	Q6CST7_KLULA	2	Q6cst7	kluyveromyc
502	126	5.7	1014	Q8QS56_9BETA	2	Q8qs56	pongine her
503	126	5.7	1266	Q626F7_CAEBR	2	Q626f7	caenorhabdi
504	126	5.7	1464	Q6CYA9_KLULA	2	Q6cya9	kluyveromyc
505	125.5	5.7	317	Q29070_PIG	2	Q29070	sus scrofa
506	125.5	5.7	345	Q5TXN7_ANOGA	2	Q5txn7	anopheles g
507	125.5	5.7	493	Q58SI9_DROSI	2	Q58si9	drosophila
508	125.5	5.7	582	Q25V62_MYCO	2	Q25v62	mycobacteri
509	125.5	5.7	588	Q9VGA8_DROME	2	Q9vga8	drosophila
510	125.5	5.7	594	Q1TG37_9MYCO	2	Q1tg37	mycobacteri
511	125.5	5.7	594	Q1TW92_9MYCO	2	Q1tw92	mycobacteri
512	125.5	5.7	594	Q1BF12_9MYCO	2	Q1bf12	mycobacteri
513	125.5	5.7	620	O07239_MYCTU	2	O07239	mycobacteri
514	125.5	5.7	629	Q59SK6_CANAL	2	Q59sk6	candida alb
515	125.5	5.7	909	LDLR1_XENLA	2	LDLR1_XENLA	xenopus lae
516	125.5	5.7	1107	Q54Z23_DICDI	2	Q54z23	dictyosteli
517	125.5	5.7	1266	Q6CAR3_YARLI	2	Q6car3	yarrowia li
518	125.5	5.7	1301	Q9VZ81_DROME	2	Q9vz81	drosophila
519	125.5	5.7	1630	Q1H8S8_YEAST	2	Q1h8s8	saccharomyc
520	125.5	5.7	2176	Q54VP0_DICDI	2	Q54vp0	dictyosteli
521	125.5	5.7	2356	Q4N3W2_THEPA	2	Q4n3w2	theileria p
522	125.5	5.7	4167	ALMS1_HUMAN	2	ALMS1_HUMAN	homo sapien
523	125	5.7	219	Q7PK77_ANOGA	2	Q7pk77	anopheles g
524	125	5.7	235	Q63349_RAT	2	Q63349	rattus norv
525	125	5.7	273	Q61002_MOUSE	2	Q61002	mus musculu
526	125	5.7	322	Q6TXG0_RAT	2	Q6txg0	rattus norv
527	125	5.7	325	Q8NAK1_HUMAN	2	Q8nak1	homo sapien
528	125	5.7	388	Q60KQ3_CAEBR	2	Q60kq3	caenorhabdi
529	125	5.7	428	Q622U1_CAEBR	2	Q622u1	caenorhabdi
530	125	5.7	585	Q58SH0_DROSI	2	Q58sh0	drosophila
531	125	5.7	585	Q58SG3_DROSI	2	Q58sg3	drosophila
532	125	5.7	585	Q58SG5_DROSI	2	Q58sg5	drosophila
533	125	5.7	589	O43419_HUMAN	2	O43419	homo sapien
534	125	5.7	600	SP96_DICDI	1	P14328	dictyosteli
535	125	5.7	678	Q54U48_DICDI	2	Q54u48	dictyosteli
536	125	5.7	812	Q61KE5_CAEBR	2	Q61ke5	caenorhabdi
537	125	5.7	961	Q92223_EMENI	2	Q92223	emericella
538	125	5.7	1089	Q54YP1_DICDI	2	Q54yp1	dictyosteli
539	125	5.7	4782	Q8KIG6_MOUSE	2	Q8kig6	mus musculu
540	124.5	5.6	404	Q5BEU7_EMENI	2	Q5beu7	emericella
541	124.5	5.6	426	Q2GZQ0_CHAGB	2	Q2gzq0	chaetomium
542	124.5	5.6	451	Q95144_CERAE	2	Q95144	cercopithec

Left column of the page (rows 543–615):

No.	Score	pI	Accession	Type	Length	Organism
543	124.5	5.6	Q9NAX4_DICDI	2	464	dictyosteli
544	124.5	5.6	Q54YL6_DICDI	2	464	dictyosteli
545	124.5	5.6	LRP11_HUMAN	1	500	homo sapien
546	124.5	5.6	Q63655_RAT	2	534	rattus norv
547	124.5	5.6	Q19780_CAEEL	2	624	caenorhabdi
548	124.5	5.6	Q8VOL3_9ALPH	2	703	equid herpe
549	124.5	5.6	Q299Y3_DROPS	2	755	drosophila
550	124.5	5.6	Q8VOL2_9ALPH	2	779	equid herpe
551	124.5	5.6	YKO2_SCHPO	1	1082	schizosacch
552	124.5	5.6	Q4DEV9_TRYCR	2	1087	trypanosoma
553	124.5	5.6	Q94248_CAEEL	2	1147	caenorhabdi
554	124.5	5.6	MSB2_YEAST	1	1306	saccharomyc
555	124.5	5.6	O55225_MOUSE	2	2910	mus musculu
556	124.5	5.6	Q5EGP2_HUMAN	2	3080	homo sapien
557	124	5.6	Q6C978_YARLI	2	376	yarrowia li
558	124	5.6	Q58SL1_DROSI	2	495	drosophila
559	124	5.6	Q58SG9_DROSI	2	582	drosophila
560	124	5.6	Q58SH3_DROSI	2	582	drosophila
561	124	5.6	Q58SG7_DROSI	2	582	drosophila
562	124	5.6	Q58SG8_DROSI	2	582	drosophila
563	124	5.6	Q5CEB1_CRYHO	2	732	cryptospori
564	124	5.6	Q54FU3_DICDI	2	732	dictyosteli
565	124	5.6	Q5B9X1_EMENI	2	864	emericella
566	124	5.6	Q20253_CAEEL	2	896	caenorhabdi
567	124	5.6	O74346_SCHPO	2	948	schizosacch
568	124	5.6	Q2PIQ6_ASPOR	2	1070	aspergillus
569	124	5.6	Q7PMD5_ANOGA	2	1113	anopheles g
570	124	5.6	Q6CBR5_YARLI	2	1136	yarrowia li
571	124	5.6	Q4I733_GIBZE	2	1170	gibberella
572	124	5.6	Q6FUJ4_CANGA	2	1185	candida gla
573	124	5.6	Q4CVS5_TRYCR	2	1204	trypanosoma
574	124	5.6	Q99208_YEAST	2	1205	saccharomyc
575	124	5.6	Q7SAF1_NEUCR	2	1217	neurospora
576	124	5.6	YMN3_YEAST	1	1374	saccharomyc
577	124	5.6	Q6CHJ5_YARLI	2	1447	yarrowia li
578	124	5.6	MUC2_RAT	1	1513	rattus norv
579	124	5.6	Q60RK8_CAEBR	2	1598	caenorhabdi
580	124	5.6	YRF12_YEAST	1	1681	saccharomyc
581	124	5.6	Q6FS79_CANGA	2	1785	candida gla
582	124	5.6	Q4SVZ2_TETNG	2	1803	tetraodon n
583	124	5.6	YRF13_YEAST	1	1859	saccharomyc
584	124	5.6	YRF16_YEAST	1	1859	saccharomyc
585	123.5	5.6	Q4CUV4_TRYCR	2	155	trypanosoma
586	123.5	5.6	Q5B1I3_EMENI	2	271	emericella
587	123.5	5.6	O18984_CERAE	2	460	cercopithec
588	123.5	5.6	Q8VIQ4_MOUSE	2	465	mus musculu
589	123.5	5.6	Q5CVA2_CRYPV	2	475	cryptospori
590	123.5	5.6	PODXL_MOUSE	1	503	mus musculu
591	123.5	5.6	Q791G4_MOUSE	2	503	mus musculu
592	123.5	5.6	GP10_DICDI	1	544	dictyosteli
593	123.5	5.6	Q55FB7_DICDI	2	544	dictyosteli
594	123.5	5.6	Q6AW05_CAEEL	2	586	caenorhabdi
595	123.5	5.6	Q1GZU2_METFL	2	586	methylobaci
596	123.5	5.6	Q99K60_MOUSE	2	631	mus musculu
597	123.5	5.6	Q8TG00_ASPFU	2	700	aspergillus
598	123.5	5.6	Q21027_CAEEL	2	786	caenorhabdi
599	123.5	5.6	Q5SW65_HUMAN	2	904	homo sapien
600	123.5	5.6	Q3DVC9_STRAG	2	910	streptococc
601	123.5	5.6	Q7WYN3_9CLOT	2	942	acetivibrio
602	123.5	5.6	Q6AW06_CAEEL	2	946	caenorhabdi
603	123.5	5.6	LRP8_HUMAN	1	963	homo sapien
604	123.5	5.6	Q5SW67_HUMAN	2	963	homo sapien
605	123.5	5.6	Q8DYL7_STRAS	2	970	streptococc
606	123.5	5.6	Q5AJV5_CANAL	2	1114	candida alb
607	123.5	5.6	Q5TMT7_ANOGA	2	1132	anopheles g
608	123.5	5.6	Q5YPQ7_NOCFA	2	1367	nocardia fa
609	123.5	5.6	Q23R53_TETTH	2	1588	tetrahymena
610	123.5	5.6	Q757A9_NEUCR	2	2076	neurospora
611	123.5	5.6	Q96U11_NEUCR	2	2117	neurospora
612	123.5	5.6	Q61T94_CAEBR	2	2119	caenorhabdi
613	123.5	5.6	Q939N5_STRGN	2	3072	streptococc
614	123	5.6	Q9PI6_PICRU	2	165	picea ruben
615	123	5.6	Q3FA55_9BURK	2	221	burkholderi

Right column of the page (rows 616–688):

No.	AC	Organism	Entry	Type	Length	pI	Score
616	Q96d42	homo sapien	TIMD1_HUMAN	1	359	5.6	123
617	Q02496	mus musculu	MUC1_MOUSE	1	630	5.6	123
618	Q7psi0	anopheles g	Q7PSI0_ANOGA	2	661	5.6	123
619	Q4wc06	aspergillus	Q4WC06_ASPFU	2	662	5.6	123
620	Q4r7t2	macaca fasc	Q4R7T2_MACFA	2	703	5.6	123
621	Q7rxd6	neurospora	Q7RXD6_NEUCR	2	719	5.6	123
622	Q6cnv3	kluyveromyc	Q6CNV3_KLULA	2	782	5.6	123
623	Q617y9	caenorhabdi	Q617Y9_CAEBR	2	791	5.6	123
624	Q2txl8	aspergillus	Q2TXL8_ASPOR	2	856	5.6	123
625	Q615w4	caenorhabdi	Q615W4_CAEBR	2	862	5.6	123
626	Q90505	fundulus he	Q90505_FUNHE	2	951	5.6	123
627	Q9rzq3	deinococcus	Q9RZQ3_DEIRA	2	1067	5.6	123
628	Q9n5k0	caenorhabdi	Q9N5K0_CAEEL	2	1203	5.6	123
629	Q3k052	streptococc	Q3K052_STRA1	2	1258	5.6	123
630	Q5alj8	candida alb	Q5ALJ8_CANAL	2	1311	5.6	123
631	Q4pee5	ustilago ma	Q4PEE5_USTMA	2	1723	5.6	123
632	Q9vel9	drosophila	Q9VEL9_DROME	2	2112	5.6	123
633	Q4pfy0	ustilago ma	Q4PFY0_USTMA	2	2193	5.6	123
634	Q54xa2	dictyosteli	Q54XA2_DICDI	2	2242	5.6	123
635	Q4fx62	leishmania	Q4FX62_LEIMA	2	17392	5.6	123
636	O43420	homo sapien	O43420_HUMAN	2	338	5.5	122.5
637	Q6bcl3	bursaphelen	Q6BCL3_BURXY	2	359	5.5	122.5
638	Q4hv72	gibberella	Q4HV72_GIBZE	2	424	5.5	122.5
639	Q5kcr5	cryptococcu	Q5KCR5_CRYNE	2	453	5.5	122.5
640	P53189	saccharomyc	SCW11_YEAST	1	542	5.5	122.5
641	Q9kjj3	enterococcu	Q9KJJ3_ENTHR	2	576	5.5	122.5
642	Q4whj8	aspergillus	Q4WHJ8_ASPFU	2	591	5.5	122.5
643	Q2bjb2	oceanospiri	Q2BJB2_9GAMM	2	648	5.5	122.5
644	Q6cbu0	yarrowia li	Q6CBU0_YARLI	2	812	5.5	122.5
645	Q5kam9	cryptococcu	Q5KAM9_CRYNE	2	861	5.5	122.5
646	Q17b16	aedes aegyp	Q17B16_AEDAE	2	904	5.5	122.5
647	Q3dkl3	streptococc	Q3DKL3_STRAG	2	931	5.5	122.5
648	Q8int1	drosophila	Q8INT1_DROME	2	976	5.5	122.5
649	Q5ajh8	candida alb	Q5AJH8_CANAL	2	1116	5.5	122.5
650	Q6f3a8	oryza sativ	Q6F3A8_ORYSA	2	1184	5.5	122.5
651	Q54y47	dictyosteli	Q54Y47_DICDI	2	1275	5.5	122.5
652	Q5alt5	candida alb	Q5ALT5_CANAL	2	1409	5.5	122.5
653	Q2w0n1	magnetospir	Q2W0N1_MAGMM	2	4218	5.5	122.5
654	Q55eg2	dictyosteli	Q55EG2_DICDI	2	4540	5.5	122.5
655	Q9erb8	mus musculu	Q9ERB8_MOUSE	2	232	5.5	122
656	Q8iqx2	drosophila	Q8IQX2_DROME	2	285	5.5	122
657	Q5k8s4	cryptococcu	Q5K8S4_CRYNE	2	311	5.5	122
658	Q55lz4	cryptococcu	Q55LZ4_CRYNE	2	311	5.5	122
659	Q3w144	frankia sp.	Q3W144_9ACTO	2	537	5.5	122
660	Q6c2k2	yarrowia li	Q6C2K2_YARLI	2	599	5.5	122
661	Q8nb72	homo sapien	Q8NB72_HUMAN	2	619	5.5	122
662	Q5b952	emericella	Q5B952_EMENI	2	730	5.5	122
663	Q9v515	drosophila	Q9V515_DROME	2	746	5.5	122
664	Q91969	gallus gall	Q91969_CHICK	2	807	5.5	122
665	Q5u94	mamestra co	Q5U94_9NEOP	2	811	5.5	122
666	Q55d98	dictyosteli	Q55D98_DICDI	2	812	5.5	122
667	Q9vs84	drosophila	Q9VS84_DROME	2	817	5.5	122
668	Q86p15	drosophila	Q86P15_DROME	2	817	5.5	122
669	Q55gh4	dictyosteli	Q55GH4_DICDI	2	878	5.5	122
670	Q4p7e4	ustilago ma	Q4P7E4_USTMA	2	928	5.5	122
671	Q28139	bos taurus	NCKX1_BOVIN	1	1216	5.5	122
672	Q54sh1	dictyosteli	Q54SH1_DICDI	2	1346	5.5	122
673	Q95re5	drosophila	Q95RE5_DROME	2	1486	5.5	122
674	Q967y2	drosophila	Q967Y2_DROME	2	1486	5.5	122
675	Q7krp7	drosophila	Q7KRP7_DROME	2	1486	5.5	122
676	Q7krp6	drosophila	Q7KRP6_DROME	2	1582	5.5	122
677	Q54bu8	dictyosteli	Q54BU8_DICDI	2	1623	5.5	122
678	Q9v918	drosophila	Q9V918_DROME	2	1976	5.5	122
679	Q8vq99	staphylococ	Q8VQ99_STAAU	2	2283	5.5	122
680	Q299y6	drosophila	Q299Y6_DROPS	2	2906	5.5	122
681	Q8v0k4	equid herpe	Q8V0K4_9ALPH	2	201	5.5	121.5
682	Q923d3	mus musculu	PARM1_MOUSE	1	296	5.5	121.5
683	Q1ivm2	acidobacter	Q1IVM2_ACIBL	2	497	5.5	121.5
684	Q81p4	saccharomyc	Q8J1P4_SACPA	2	576	5.5	121.5
685	Q81p3	saccharomyc	Q8J1P3_SACPA	2	585	5.5	121.5
686	Q8j0c8	saccharomyc	Q8J0C8_SACPA	2	598	5.5	121.5
687	Q1fat2	roseiflexus	Q1FAT2_9CHLR	2	599	5.5	121.5
688	Q81p2	saccharomyc	Q8J1P2_SACPA	2	601	5.5	121.5

No.			Length	Count	ID	Organism
689	121.5	5.5	702	2	Q96PX1_HUMAN	homo sapien
690	121.5	5.5	763	2	Q5A8K3_CANAL	candida alb
691	121.5	5.5	831	2	Q6C5E4_YARLI	yarrowia li
692	121.5	5.5	866	2	Q752V0_ASHGO	ashbya goss
693	121.5	5.5	888	2	Q25336_LEIME	leishmania
694	121.5	5.5	954	2	Q61OZ8_CAEBR	caenorhabdi
695	121.5	5.5	1035	2	Q2H6W9_CHAGB	chaetomium
696	121.5	5.5	1041	2	EGT2_YEAST	saccharomyc
697	121.5	5.5	1058	2	Q54KS2_DICDI	dictyosteli
698	121.5	5.5	1068	2	Q5BJ28_MOUSE	mus musculu
699	121.5	5.5	1179	2	Q8WR08_DROME	drosophila
700	121.5	5.5	1208	2	Q2IZL3_DROPS	drosophila
701	121.5	5.5	1535	2	Q5SJZ9_CRYNE	cryptococcu
702	121.5	5.5	1535	2	Q5K9K1_CRYNE	cryptococcu
703	121.5	5.5	1814	2	Q4P858_USTMA	ustilago ma
704	121.5	5.5	1854	2	Q7ZA78_CANAL	candida alb
705	121.5	5.5	2432	2	Q1IF85_9PSED	pseudomonas
706	121.5	5.5	2722	2	Q55A92_DICDI	dictyosteli
707	121.5	5.5	2722	2	Q86JN0_DICDI	dictyosteli
708	121.5	5.5	4776	2	Q97P71_STRPN	streptococc
709	121.5	5.5	5301	2	Q16VU7_AEDAE	aedes aegyp
710	121	5.5	216	2	Q28501_MACMU	macaca mula
711	121	5.5	316	2	Q9U9J0_TOXCA	toxocara ca
712	121	5.5	402	2	O23054_ARATH	arabidopsis
713	121	5.5	452	2	Q17LZ1_AEDAE	aedes aegyp
714	121	5.5	495	2	Q58SJ9_DROSI	drosophila
715	121	5.5	520	2	O84054_CHLTR	chlamydia t
716	121	5.5	583	2	Q1BEL2_9MYCO	mycobacteri
717	121	5.5	585	2	Q58SH2_DROSI	drosophila
718	121	5.5	600	2	Q86B01_DICDI	dictyosteli
719	121	5.5	600	2	Q550K7_DICDI	dictyosteli
720	121	5.5	603	2	Q6CE49_YARLI	yarrowia li
721	121	5.5	609	2	Q1TDL3_9MYCO	mycobacteri
722	121	5.5	657	2	Q5AZW9_EMENI	emericella
723	121	5.5	667	2	Q2UIE6_ASPOR	aspergillus
724	121	5.5	695	2	Q4X3F3_PLACH	plasmodium
725	121	5.5	714	2	Q59TP1_CANAL	candida alb
726	121	5.5	714	2	Q59TK9_CANAL	candida alb
727	121	5.5	730	2	Q4FWC2_LEIMA	leishmania
728	121	5.5	732	2	Q4I7J9_GIBZE	gibberella
729	121	5.5	750	2	Q9HFZ4_CANAL	candida alb
730	121	5.5	863	2	Q54Q23_DICDI	dictyosteli
731	121	5.5	874	2	Q8JIS6_BRARE	brachydanio
732	121	5.5	916	2	Q7YZI0_MONBE	monosiga br
733	121	5.5	944	2	Q9UP82_HUMAN	homo sapien
734	121	5.5	957	2	Q9UKN0_HUMAN	homo sapien
735	121	5.5	957	2	O14651_HUMAN	homo sapien
736	121	5.5	997	2	Q93804_YEAST	saccharomyc
737	121	5.5	1028	2	Q4I6A6_KINRA	kineococcus
738	121	5.5	1045	2	O76037_HUMAN	homo sapien
739	121	5.5	1140	2	Q4PHD3_USTMA	ustilago ma
740	121	5.5	1200	2	PO121_MOUSE	mus musculu
741	121	5.5	1200	2	Q3U425_MOUSE	mus musculu
742	121	5.5	1224	2	Q3E7W8_YEAST	saccharomyc
743	121	5.5	1382	2	YRF14_YEAST	saccharomyc
744	121	5.5	1625	2	Q6MVD4_NEUCR	neurospora
745	121	5.5	1627	2	Q7R446_GIALA	giardia lam
746	121	5.5	1763	2	Q8I1I0_CAEEL	caenorhabdi
747	121	5.5	1796	1	YRF11_YEAST	saccharomyc
748	121	5.5	1829	2	Q22248_CAEEL	caenorhabdi
749	121	5.5	2963	2	Q7PQY5_ANOGA	anopheles g
750	120.5	5.5	3008	2	Q60MN8_CAEBR	caenorhabdi
751	120.5	5.5	189	2	Q4CTP5_TRYCR	trypanosoma
752	120.5	5.5	240	2	Q8V0K5_9ALPH	equid herpe
753	120.5	5.5	264	2	Q80X55_MOUSE	mus musculu
754	120.5	5.5	268	2	Q4QEM8_LEIMA	leishmania
755	120.5	5.5	323	2	Q1WTD2_LACS1	lactobacill
756	120.5	5.5	402	2	Q9N503_CAEEL	caenorhabdi
757	120.5	5.5	402	2	O44626_CAEEL	caenorhabdi
758	120.5	5.5	429	2	Q5X143_LEGPA	legionella
759	120.5	5.5	471	2	Q9VMG7_DROME	drosophila
760	120.5	5.5	547	2	Q4QGL5_LEIMA	leishmania
761	120.5	5.5	548	2	Q1FDP7_9CHLR	roseiflexus

Accession	Organism	ID	Count	Length			No.
Q4p7c8	ustilago ma	Q4P7C8_USTMA	2	569	5.5	120.5	762
Q5u2x9	rattus norv	Q5U2X9_RAT	2	678	5.5	120.5	763
P04065	saccharomy	AMYH_SACDI	1	767	5.5	120.5	764
Q8v0l1	equid herpe	Q8V0L1_9ALPH	2	804	5.5	120.5	765
Q758m4	ashbya goss	Q758M4_ASHGO	2	805	5.5	120.5	766
Q54j73	dictyosteli	Q54J73_DICDI	2	809	5.5	120.5	767
Q3kst4	epstein-bar	Q3KST4_EBVG	2	856	5.5	120.5	768
Q9w4a6	drosophila	Q9W4A6_DROME	2	916	5.5	120.5	769
Q60q42	caenorhabdi	Q60Q42_CAEBR	2	972	5.5	120.5	770
Q4sfn0	tetraodon n	Q4SFN0_TETNG	1	1095	5.5	120.5	771
P36170	saccharomyc	YK82_YEAST	1	1169	5.5	120.5	772
Q54hl3	dictyosteli	Q54HL3_DICDI	2	1200	5.5	120.5	773
Q8e473	streptococc	Q8E473_STRA3	2	1310	5.5	120.5	774
Q3d424	streptococc	Q3D424_STRAG	2	1326	5.5	120.5	775
Q55mk2	cryptococcu	Q55MK2_CRYNE	2	1409	5.5	120.5	776
Q757n5	ashbya goss	Q757N5_ASHGO	2	1458	5.5	120.5	777
Q1xbs9	bovine herp	Q1XBS9_BHV4	2	269	5.4	120	778
Q8v0k0	equid herpe	Q8V0K0_9ALPH	2	273	5.4	120	779
P87519	bovine herp	P87519_BHV4	2	273	5.4	120	780
Q5raf8	pongo pygma	PARM1_PONPY	1	310	5.4	120	781
Q1tr68	mycobacteri	Q1TR68_9MYCO	2	382	5.4	120	782
P15702	mus musculu	LEUK_MOUSE	1	395	5.4	120	783
Q544c5	mus musculu	Q544C5_MOUSE	2	395	5.4	120	784
Q6c2x8	yarrowia li	Q6C2X8_YARLI	2	461	5.4	120	785
Q09586	caenorhabdi	Q09586_CAEEL	2	488	5.4	120	786
Q7z434	h mitochond	MAVS_HUMAN	1	540	5.4	120	787
Q2hwt5	homo sapien	Q2HWT5_HUMAN	2	540	5.4	120	788
Q35818	bradyrhizob	Q35818_9BRAD	2	567	5.4	120	789
Q62223	caenorhabdi	Q62223_CAEEL	2	575	5.4	120	790
Q9n2v0	caenorhabdi	Q9N2V0_CAEEL	2	665	5.4	120	791
Q6mrj7	bdellovibri	Q6MRJ7_BDEBA	2	685	5.4	120	792
Q4p0g8	ustilago ma	Q4P0G8_USTMA	2	735	5.4	120	793
O39307	equid herpe	O39307_9ALPH	2	750	5.4	120	794
Q9u6m6	loligo peal	Q9U6M6_LOLPE	2	751	5.4	120	795
Q86ag3	dictyosteli	Q86AG3_DICDI	2	762	5.4	120	796
Q9hci5	homo sapien	MAGE1_HUMAN	1	957	5.4	120	797
Q5jxc7	homo sapien	Q5JXC7_HUMAN	1	957	5.4	120	798
Q55de7	dictyosteli	Q55DE7_DICDI	2	1103	5.4	120	799
Q554h8	dictyosteli	Q554H8_DICDI	2	1123	5.4	120	800
Q86i06	dictyosteli	Q86I06_DICDI	2	1123	5.4	120	801
Q60nc3	caenorhabdi	Q60NC3_CAEBR	2	1165	5.4	120	802
Q9ukw9	homo sapien	Q9UKW9_HUMAN	2	1217	5.4	120	803
Q8wpv5	schistosoma	Q8WPV5_SCHMA	2	1264	5.4	120	804
Q559h2	dictyosteli	Q559H2_DICDI	2	1309	5.4	120	805
Q86jc1	dictyosteli	Q86JC1_DICDI	2	1309	5.4	120	806
Q6w4x9	homo sapien	Q6W4X9_HUMAN	2	1569	5.4	120	807
Q7za79	candida alb	Q7ZA79_CANAL	2	1833	5.4	120	808
Q7ytp1	caenorhabdi	Q7YTP1_CAEBL	2	174	5.4	119.5	809
Q5v8a3	saccharomyc	Q5V8A3_SACBA	2	246	5.4	119.5	810
Q9ytl5	ateline her	Q9YTL5_ATHV3	2	349	5.4	119.5	811
Q88ts6	lactobacill	Q88TS6_LACPL	2	354	5.4	119.5	812
Q7tfj3	rhesus cyto	Q7TFJ3_RHCM6	2	356	5.4	119.5	813
Q669s7	yersinia ps	Q669S7_YERPS	2	439	5.4	119.5	814
Q38z86	lactobacill	Q38Z86_LACSS	2	448	5.4	119.5	815
Q8nc85	homo sapien	Q8NC85_HUMAN	2	470	5.4	119.5	816
Q8nbs8	homo sapien	Q8NBS8_HUMAN	2	470	5.4	119.5	817
Q9xuf4	caenorhabdi	Q9XUF4_CAEBL	2	481	5.4	119.5	818
Q5z3r8	nocardia fa	Q5Z3R8_NOCFA	2	507	5.4	119.5	819
Q2kjj7	bos taurus	Q2KJJ7_BOVIN	2	513	5.4	119.5	820
Q9fyw4	lycopersico	Q9FYW4_LYCES	2	519	5.4	119.5	821
Q54b97	dictyosteli	Q54B97_DICDI	2	524	5.4	119.5	822
P19467	mus musculu	MUC13_MOUSE	1	573	5.4	119.5	823
Q3v1s6	mus musculu	Q3V1S6_MOUSE	2	573	5.4	119.5	824
Q4hv75	gibberella	Q4HV75_GIBZE	2	719	5.4	119.5	825
Q1ydx1	aurantimona	Q1YDX1_9RHIZ	2	734	5.4	119.5	826
O91331	cercopithmona	O91331_9GAMA	2	783	5.4	119.5	827
Q9w3k6	drosophila	Q9W3K6_DROME	2	801	5.4	119.5	828
Q9qp87	epstein-bar	Q9QP87_EBVG	2	886	5.4	119.5	829
Q4pi38	ustilago ma	Q4PI38_USTMA	2	1014	5.4	119.5	830
Q07888	saccharomyc	Q07888_YEAST	2	1205	5.4	119.5	831
Q55ff5	dictyosteli	Q55FF5_DICDI	2	1537	5.4	119.5	832
Q1u6w4	lactobacill	Q1U6W4_LACRE	2	1627	5.4	119.5	833
Q7kt96	drosophila	Q7KT96_DROME	2	1853	5.4	119.5	834

No	Score1	Score2	Length	Cnt	Name	Organism	Accession
835	119.5	5.4	2523	2	Q41EB9_GIBZE	gibberella	Q4iEB9
836	119.5	5.4	2625	2	Q8MMZ9_DICDI	dictyosteli	Q8mmz9
837	119.5	5.4	2625	2	Q54ZL7_DICDI	dictyosteli	Q54zl7
838	119.5	5.4	2800	2	Q6XHB1_DICDI	dictyosteli	Q6xhb1
839	119.5	5.4	6995	2	Q8FQU3_COREF	corynebacte	Q8fqu3
840	119	5.4	178	2	Q29EG0_DROPS	drosophila	Q29eg0
841	119	5.4	185	2	Q98TQ9_CHICK	gallus gall	Q98tq9
842	119	5.4	215	2	Q1RX73_MEDTR	medicago tr	Q1rx73
843	119	5.4	222	2	Q54E70_DICDI	dictyosteli	Q54e70
844	119	5.4	229	2	Q5CRW5_CRYPV	cryptospori	Q5crw5
845	119	5.4	354	2	Q8K5B0_RAT	rattus norv	Q8k5b0
846	119	5.4	420	2	Q3E681_CHLAU	chloroflexu	Q3e681
847	119	5.4	437	2	(illegible)	homo sapien	(illegible)
848	119	5.4	475	1	MUC1_HYLLA	hylobates l	
849	119	5.4	490	2	Q753Y1_ASHGO	ashbya goss	Q753y1
850	119	5.4	491	2	Q9BIQ4_9BILA	cooperia pu	Q9biq4
851	119	5.4	507	2	Q59JP5_CANAL	candida alb	Q59jp5
852	119	5.4	520	2	Q5CW96_CRYPV	cryptospori	Q5cw96
853	119	5.4	560	2	Q76183_HUMAN	homo sapien	Q76183
854	119	5.4	560	2	Q5YN12_NOCFA	nocardia fa	Q5yn12
855	119	5.4	601	2	Q9CII3_CANAL	candida alb	Q9cii3
856	119	5.4	609	2	Q1TWP1_9MYCO	mycobacteri	Q1twp1
857	119	5.4	610	1	MUC4_HUMAN	homo sapien	
858	119	5.4	636	2	Q7S4N7_NEUCR	neurospora	Q7s4n7
859	119	5.4	636	2	Q53KW1_ORYSA	oryza sativ	Q53kw1
860	119	5.4	663	2	Q3HVK1_9EUKA	monosiga ov	Q3hvk1
861	119	5.4	715	2	Q4SPW5_TETNG	tetraodon n	Q4spw5
862	119	5.4	755	2	Q54CM9_DICDI	dictyosteli	Q54cm9
863	119	5.4	768	1	AMY1_SACDI	saccharomyc	
864	119	5.4	791	2	Q59ED4_HUMAN	homo sapien	Q59ed4
865	119	5.4	823	2	Q6C159_YARLI	yarrowia li	Q6c159
866	119	5.4	825	2	Q8V0L0_9ALPH	equid herpe	Q8v0l0
867	119	5.4	828	2	Q4ZH58_MICOE	microtus oe	Q4zh58
868	119	5.4	856	2	Q7XZZ2_ORYSA	oryza sativ	Q7xzz2
869	119	5.4	936	2	Q6FTU1_CANGA	candida gla	Q6ftu1
870	119	5.4	996	1	LRP8_MOUSE	mus musculu	
871	119	5.4	1159	2	Q1F1W2_9CHLR	roseiflexus	Q1f1w2
872	119	5.4	1176	2	Q59SD7_CANAL	candida alb	Q59sd7
873	119	5.4	1255	2	Q54HF3_DICDI	dictyosteli	Q54hf3
874	119	5.4	1279	2	Q6PAC4_MOUSE	mus musculu	Q6pac4
875	119	5.4	1350	2	Q80220_MOUSE	mus musculu	Q80220
876	119	5.4	1363	2	Q2UUR2_ASPOR	aspergillus	Q2uur2
877	119	5.4	1467	2	Q29AL0_DROPS	drosophila	Q29al0
878	118.5	5.4	2174	2	Q6CD35_YARLI	yarrowia li	Q6cd35
879	118.5	5.4	5017	2	Q63DF3_BACCZ	bacillus ce	Q63df3
880	118.5	5.4	222	2	Q86918_BABMI	babesia mic	Q86918
881	118.5	5.4	232	2	Q27423_DROVI	drosophila	Q27423
882	118.5	5.4	269	2	Q9U9J2_TOXCA	toxocara ca	Q9u9j2
883	118.5	5.4	294	2	Q99322_HUMAN	homo sapien	Q99322
884	118.5	5.4	376	2	Q6DTM8_CANGA	candida gla	Q6dtm8
885	118.5	5.4	393	2	Q5KES3_CRYNE	cryptococcu	Q5kes3
886	118.5	5.4	396	2	Q55RR7_CRYNE	cryptococcu	Q55rr7
887	118.5	5.4	437	2	Q567K3_BRARE	brachydanio	Q567k3
888	118.5	5.4	463	2	Q6FW57_CANGA	candida gla	Q6fw57
889	118.5	5.4	507	2	O13028_BORSA	boreogadus	O13028
890	118.5	5.4	562	1	GUN1_ACICE	acidothermu	
891	118.5	5.4	562	2	Q2E2T3_ACICE	acidothermu	Q2e2t3
892	118.5	5.4	616	2	Q4WC60_ASPFU	aspergillus	Q4wc60
893	118.5	5.4	695	2	Q2U6F7_ASPOR	aspergillus	Q2u6f7
894	118.5	5.4	707	2	O00839_LEIDO	leishmania	O00839
895	118.5	5.4	719	2	Q4KLV9_XENLA	xenopus lae	Q4klv9
896	118.5	5.4	721	2	Q6DDN6_XENLA	xenopus lae	Q6ddn6
897	118.5	5.4	745	2	Q3E0G9_CHLAU	chloroflexu	Q3e0g9
898	118.5	5.4	770	2	Q4PFX2_USTMA	ustilago ma	Q4pfx2
899	118.5	5.4	840	2	Q54VZ5_DICDI	dictyosteli	Q54vz5
900	118.5	5.4	928	2	Q98906_CHICK	gallus gall	Q98906
901	118.5	5.4	972	2	Q54CN0_DICDI	dictyosteli	Q54cn0
902	118.5	5.4	995	1	YIQ9_YEAST	saccharomyc	P40442
903	118.5	5.4	1055	2	Q833R5_ENTFA	enterococcu	Q833r5
904	118.5	5.4	1118	2	Q28226_CANFA	canis famil	Q28226
905	118.5	5.4	1126	2	Q9VGK5_DROME	drosophila	Q9vgk5
906	118.5	5.4	1256	2	Q54RH9_DICDI	dictyosteli	Q54rh9
907	118.5	5.4	1415	2	Q5JV36_HUMAN	homo sapien	Q5jv36
908	118.5	5.4	1497	1	COHA1_HUMAN	homo sapien	Q9umd9
909	118.5	5.4	1563	1	YJP1_SCHPO	schizosacch	Q9p6s0
910	118.5	5.4	1838	2	Q960G3_DROME	drosophila	Q960g3
911	118	5.3	165	2	Q26877_TRYCR	trypanosoma	Q26877
912	118	5.3	288	2	Q1UKM6_ASPOR	aspergillus	Q1ukm6
913	118	5.3	343	2	Q1U9W2_LACRE	lactobacill	Q1u9w2
914	118	5.3	371	2	Q5F2J0_ENCIN	encephalito	Q5f2j0
915	118	5.3	385	2	Q27E69_MYCFV	mycobacteri	Q27e69
916	118	5.3	447	2	Q297S3_DROPS	drosophila	Q297s3
917	118	5.3	481	2	Q564Z6_CAEEL	caenorhabdi	Q564z6
918	118	5.3	485	2	Q5Y2C1_9STRA	thalassiosi	Q5y2c1
919	118	5.3	496	2	Q980D5_SULSO	sulfolobus	Q980d5
920	118	5.3	503	2	Q4JLF0_LACRE	lactobacill	Q4jlf0
921	118	5.3	517	2	Q9P2I8_HUMAN	homo sapien	Q9p2i8
922	118	5.3	602	2	Q5A271_CANAL	candida alb	Q5a271
923	118	5.3	639	2	Q69Z27_MOUSE	mus musculu	Q69z27
924	118	5.3	645	2	Q2GVP6_CHAGB	chaetomium	Q2gvp6
925	118	5.3	708	2	Q7R9K7_PLAYO	plasmodium	Q7r9k7
926	118	5.3	729	2	Q5ZLE7_CHICK	gallus gall	Q5zle7
927	118	5.3	789	1	ARNT_HUMAN	homo sapien	P27540
928	118	5.3	789	2	Q5QP39_HUMAN	homo sapien	Q5qp39
929	118	5.3	849	2	Q8NDC7_HUMAN	homo sapien	Q8ndc7
930	118	5.3	853	2	Q4Q3E7_LEIMA	leishmania	Q4q3e7
931	118	5.3	886	1	VGP3_EBVA8	epstein-bar	P68343
932	118	5.3	886	1	VGP3_EBVP3	epstein-bar	P68344
933	118	5.3	886	1	Q1HVG6_BBVG	epstein-bar	Q1hvg6
934	118	5.3	907	2	Q66537_BBVG	cryptospori	Q66537
935	118	5.3	956	2	O00908_CRYPV	caenorhabdi	O00908
936	118	5.3	1000	2	Q5QH6_CAEEL	homo sapien	Q5qh6
937	118	5.3	1005	2	Q5JPC9_HUMAN	mus musculu	Q5jpc9
938	118	5.3	1042	2	Q80ZZ9_MOUSE	candida alb	Q80zz9
939	118	5.3	1048	2	Q59SE0_CANAL	candida alb	Q59se0
940	118	5.3	1048	2	Q59SH1_CANAL	gallus gall	Q59sh1
941	118	5.3	1057	2	Q5F3U0_CHICK	candida alb	Q5f3u0
942	118	5.3	1087	2	Q59X60_CANAL	homo sapien	Q59x60
943	118	5.3	1107	2	Q9H4D6_HUMAN	streptococc	Q9h4d6
944	118	5.3	1130	2	Q3DFZ9_STRAG	mus musculu	Q3dfz9
945	118	5.3	1153	2	Q8BQ40_MOUSE	homo sapien	Q8bq40
946	118	5.3	1157	2	Q9GZM2_HUMAN	homo sapien	Q9gzm2
947	118	5.3	1187	2	Q9GZV6_HUMAN	homo sapien	Q9gzv6
948	118	5.3	1199	2	Q9H487_HUMAN	homo sapien	Q9h487
949	118	5.3	1201	2	Q9H486_HUMAN	brachydanio	Q9h486
950	118	5.3	1209	2	Q7SZF4_BRARE	homo sapien	Q7szf4
951	118	5.3	1214	2	Q9H485_HUMAN	homo sapien	Q9h485
952	118	5.3	1215	2	Q9H484_HUMAN	trypanosoma	Q9h484
953	118	5.3	1252	2	Q4DPX0_TRYCR	homo sapien	Q4dpx0
954	118	5.3	1256	2	Q9H483_HUMAN	leishmania	Q9h483
955	118	5.3	1282	2	Q4QCU0_LEIMA	candida alb	Q4qcu0
956	118	5.3	1308	2	Q5A1E0_CANAL	aedes aegyp	Q5a1e0
957	118	5.3	1345	2	Q16WH6_AEDAE	gibberella	Q16wh6
958	118	5.3	1347	2	Q4HYE1_GIBZE	aedes aegyp	Q4hye1
959	118	5.3	1365	2	Q17AY0_AEDAE	neurospora	Q17ay0
960	118	5.3	1422	2	Q7S6K9_NEUCR	brachydanio	Q7s6k9
961	118	5.3	1436	2	Q1L8U8_BRARE	homo sapien	Q1l8u8
962	118	5.3	1827	2	Q9H482_HUMAN	xenopus lae	Q9h482
963	118	5.3	2037	2	Q9PVZ2_XENLA	homo sapien	Q9pvz2
964	118	5.3	2117	2	Q9H4D8_HUMAN	homo sapien	Q9h4d8
965	118	5.3	2167	2	Q9H481_HUMAN	homo sapien	Q9h481
966	118	5.3	2169	2	Q9NY09_HUMAN	dictyosteli	Q9ny09
967	118	5.3	2800	2	Q1ZXD6_DICDI	ustilago ma	Q1zxd6
968	118	5.3	3175	2	Q4P1K8_USTMA	leishmania	Q4p1k8
969	118	5.3	7194	2	Q4FX63_LEIMA	drosophila	Q4fx63
970	118	5.3	16223	2	Q8IR22_DROME	aedes aegyp	Q8ir22
971	117.5	5.3	182	2	Q1HRR1_AEDAE	equid herpe	Q1hrr1
972	117.5	5.3	218	2	Q8V0K3_9ALPH	caenorhabdi	Q8v0k3
973	117.5	5.3	230	2	O76597_CAEEL	plasmodium	O76597
974	117.5	5.3	250	2	Q4XLA0_PLACH	saccharomyc	Q4xla0
975	117.5	5.3	268	2	Q8J1N9_SACPA	lumbricus r	Q8j1n9
976	117.5	5.3	320	2	Q9U5N4_LUMRU	anopheles g	Q9u5n4
977	117.5	5.3	410	2	Q7P2X2_ANOGA	drosophila	Q7p2x2
978	117.5	5.3	418	2	Q9W2R6_DROME	kluyveromyc	Q9w2r6
979	117.5	5.3	419	2	Q6CX28_KLULA	yarrowia li	Q6cx28
980	117.5	5.3	487	2	Q6C575_YARLI	homo sapien	Q6c575

#	Length	pI	MW	Name	n	Accession	Organism
981	546	5.3	117.5	Q16P47_AEDAE	2	Q16p47	aedes aegyp
982	557	5.3	117.5	Q5W7D1_ORYSA	2	Q5w7d1	oryza sativ
983	565	5.3	117.5	Q73T86_MYCPA	2	Q73t86	mycobacteri
984	598	5.3	117.5	Q27CA1_MYCFV	2	Q27ca1	mycobacteri
985	668	5.3	117.5	Q16HY5_AEDAE	2	Q16hy5	aedes aegyp
986	721	5.3	117.5	Q32NX7_XENLA	2	Q32nx7	xenopus lae
987	726	5.3	117.5	Q8V0L4_9ALPH	2	Q8v0l4	equid herpe
988	735	5.3	117.5	Q1DNR2_COCIM	2	Q1dnr2	coccidioide
989	768	5.3	117.5	Q56TL1_CASSA	2	Q56tl1	castanea sa
990	821	5.3	117.5	Q5AXD9_EMENI	2	Q5axd9	emericella
991	862	5.3	117.5	Q8K0T1_MOUSE	2	Q8k0t1	mus musculu
992	907	5.3	117.5	VGP3_EBV	2	P03200	epstein-bar
993	907	5.3	117.5	Q777F0_EBVG	2	Q777f0	epstein-bar
994	1032	5.3	117.5	Q08995_YEAST	2	Q08995	saccharomyc
995	1076	5.3	117.5	Q613K9_CAEBR	2	Q613k9	caenorhabdi
996	1148	5.3	117.5	Q6CBJ2_YARLI	2	Q6cbj2	yarrowia li
997	1170	5.3	117.5	Q54PK2_DICDI	2	Q54pk2	dictyosteli
998	1223	5.3	117.5	Q68FE6_MOUSE	2	Q68fe6	mus musculu
999	1262	5.3	117.5	Q80T73_MOUSE	2	Q80t73	mus musculu
1000	1268	5.3	117.5	Q616W0_CAEBR	2	Q616w0	caenorhabdi
1001	1366	5.3	117.5	Q29M35_DROPS	2	Q29m35	drosophila
1002	1541	5.3	117.5	YHY6_YEAST	1	P38873	saccharomyc
1003	1761	5.3	117.5	JHD2B_HUMAN	1	Q71bc6	homo sapien
1004	1777	5.3	117.5	Q54FB8_DICDI	2	Q54fb8	dictyosteli
1005	1861	5.3	117.5	Q55FI2_DICDI	2	Q55fi2	dictyosteli
1006	1871	5.3	117.5	Q7QUB4_GIALA	2	Q7qub4	giardia lam
1007	2089	5.3	117.5	MDC1_HUMAN	1	Q14676	homo sapien
1008	2344	5.3	117.5	Q9N3Y8_CAEEL	2	Q9n3y8	caenorhabdi
1009	143	5.3	117	Q61Q28_TRYCR	2	Q61q28	trypanosoma
1010	273	5.3	117	Q99CZ0_BHV4	2	Q99cz0	bovine herp
1011	293	5.3	117	Q8V0K1_9ALPH	2	Q8v0k1	equid herpe
1012	303	5.3	117	Q176H7_AEDAE	2	Q176h7	aedes aegyp
1013	341	5.3	117	Q4KM82_RAT	2	Q4km82	rattus norv
1014	358	5.3	117	Q4ID92_GIBZE	2	Q4id92	gibberella
1015	358	5.3	117	Q2SSW7_SALRD	2	Q2ssw7	salinibacte
1016	367	5.3	117	Q59PF6_CANAL	2	Q59pf6	candida alb
1017	424	5.3	117	Q2FAF5_9BETA	2	Q2faf5	cercopithec
1018	440	5.3	117	Q9P566_NEUCR	2	Q9p566	neurospora
1019	551	5.3	117	YG1F_YEAST	1	P53214	saccharomyc
1020	560	5.3	117	Q59PM5_CANAL	2	Q59pm5	candida alb
1021	567	5.3	117	Q7U0V3_MYCBO	2	Q7u0v3	mycobacteri
1022	567	5.3	117	O05592_MYCTU	2	O05592	mycobacteri
1023	578	5.3	117	Q7PN14_ANOGA	2	Q7pn14	anopheles g
1024	592	5.3	117	Q23036_CAEEL	2	Q23036	caenorhabdi
1025	676	5.3	117	Q2UB58_ASPOR	2	Q2ub58	aspergillus
1026	682	5.3	117	Q7SEK6_NEUCR	2	Q7sek6	neurospora
1027	700	5.3	117	Q25884_PLAFA	2	Q25884	plasmodium
1028	760	5.3	117	Q90WR9_CHICK	2	Q90wr9	gallus gall
1029	786	5.3	117	Q86L03_DICDI	2	Q86l03	dictyosteli
1030	786	5.3	117	Q55OG3_DICDI	2	Q55og3	dictyosteli
1031	813	5.3	117	Q8IMR7_DROME	2	Q8imr7	drosophila
1032	836	5.3	117	ZHX2_MOUSE	1	Q8coco	mus musculu
1033	836	5.3	117	Q3TZR8_MOUSE	2	Q3tzr8	mus musculu
1034	874	5.3	117	Q8JIR5_BRARE	2	Q8jir5	brachydanio
1035	904	5.3	117	Q16J15_AEDAE	2	Q16j15	aedes aegyp
1036	975	5.3	117	Q962D2_DROME	2	Q962d2	drosophila
1037	1121	5.3	117	Q72884_CANAL	2	Q72884	candida alb
1038	1189	5.3	117	Q88T60_LACPL	2	Q88t60	lactobacill
1039	1253	5.3	117	Q2URG2_ASPOR	2	Q2urg2	aspergillus
1040	1327	5.3	117	Q5I6L6_SOLTU	2	Q5i6l6	solanum tub
1041	1412	5.3	117	Q9VKJ1_DROME	2	Q9vkj1	drosophila
1042	1565	5.3	117	Q8NIW5_NEUCR	2	Q8niw5	neurospora
1043	1711	5.3	117	NU214_DROME	1	Q9w1x4	drosophila
1044	1865	5.3	117	Q9HCM3_HUMAN	2	Q9hcm3	homo sapien
1045	2016	5.3	117	Q9VLS7_DROME	2	Q9vls7	drosophila
1046	2084	5.3	117	Q9HEC9_NEUCR	2	Q9hec9	neurospora
1047	2176	5.3	117	Q55BQ8_DICDI	2	Q55bq8	dictyosteli
1048	182	5.3	116.5	Q8IOD8_DROME	2	Q810d8	drosophila
1049	183	5.3	116.5	Q9VT37_DROME	2	Q9vt37	drosophila
1050	193	5.3	116.5	Q5NAP7_ORYSA	2	Q5nap7	oryza sativ
1051	278	5.3	116.5	Q14884_HUMAN	2	Q14884	homo sapien
1052	291	5.3	116.5	Q8V0K8_9ALPH	2	Q8v0k8	equid herpe
1053	323	5.3	116.5	Q4E2C2_TRYCR	2	Q4e2c2	trypanosoma
1054	335	5.3	116.5	O14652_HUMAN	2	O14652	homo sapien
1055	354	5.3	116.5	Q6PNA3_WHEAT	2	Q6pna3	triticum ae
1056	366	5.3	116.5	Q5AVE5_EMENI	2	Q5ave5	emericella
1057	384	5.3	116.5	Q614K5_CAEBR	2	Q614k5	caenorhabdi
1058	385	5.3	116.5	Q5A5T7_CANAL	2	Q5a5t7	candida alb
1059	417	5.3	116.5	Q6V4B7_DROYA	2	Q6v4b7	drosophila
1060	438	5.3	116.5	Q1F572_9CHLR	2	Q1f572	roseiflexus
1061	441	5.3	116.5	O43421_HUMAN	2	O43421	homo sapien
1062	460	5.3	116.5	Q7JPK1_DICDI	2	Q7jpk1	dictyosteli
1063	477	5.3	116.5	Q564Z7_CAEEL	2	Q564z7	caenorhabdi
1064	508	5.3	116.5	Q18951_CAEEL	2	Q18951	caenorhabdi
1065	515	5.3	116.5	Q5ADM2_CANAL	2	Q5adm2	candida alb
1066	517	5.3	116.5	Q7S8A2_NEUCR	2	Q7s8a2	neurospora
1067	559	5.3	116.5	Q9XVV1_CAEEL	2	Q9xvv1	caenorhabdi
1068	623	5.3	116.5	Q9RXB6_DEIRA	2	Q9rxb6	deinococcus
1069	746	5.3	116.5	Q6DIR2_XENTR	2	Q6dir2	xenopus tro
1070	758	5.3	116.5	Q54UR7_DICDI	2	Q54ur7	dictyosteli
1071	780	5.3	116.5	Q6CB04_YARLI	2	Q6cb04	yarrowia li
1072	804	5.3	116.5	EPC2_XENLA	1	Q66ja8	xenopus lae
1073	852	5.3	116.5	Q9VV62_DROME	2	Q9vv62	drosophila
1074	877	5.3	116.5	Q23853_DICDI	2	Q23853	dictyosteli
1075	878	5.3	116.5	Q9H3Q7_HUMAN	2	Q9h3q7	homo sapien
1076	937	5.3	116.5	Q4P7P4_USTMA	2	Q4p7p4	ustilago ma
1077	971	5.3	116.5	Q4IMB2_GIBZE	2	Q4imb2	gibberella
1078	1055	5.3	116.5	Q55G65_DICDI	2	Q55g65	dictyosteli
1079	1097	5.3	116.5	Q23AY7_TETTH	2	Q23ay7	tetrahymena
1080	1113	5.3	116.5	Q4WDJ4_ASPFU	2	Q4wdj4	aspergillus
1081	1196	5.3	116.5	Q4RP28_TETNG	2	Q4rp28	tetraodon n
1082	1197	5.3	116.5	Q298D2_DROPS	2	Q298d2	drosophila
1083	1266	5.3	116.5	Q16QT8_AEDAE	2	Q16qt8	aedes aegyp
1084	1423	5.3	116.5	Q172H6_AEDAE	2	Q172h6	aedes aegyp
1085	1440	5.3	116.5	Q4P2I2_USTMA	2	Q4p2i2	ustilago ma
1086	1692	5.3	116.5	Q7JM48_CAEEL	2	Q7jm48	caenorhabdi
1087	1997	5.3	116.5	Q5EE04_XENLA	2	Q5ee04	xenopus lae
1088	2066	5.3	116.5	Q22190_CAEEL	2	Q22190	caenorhabdi
1089	2089	5.3	116.5	Q2L6H7_MOUSE	2	Q2l6h7	mus musculu
1090	2134	5.3	116.5	Q7JM44_CAEEL	2	Q7jm44	caenorhabdi
1091	2171	5.3	116.5	Q1XHY6_PANTR	2	Q1xhy6	pan troglod
1092	2350	5.3	116.5	Q17IK9_AEDAE	2	Q17ik9	aedes aegyp
1093	3421	5.3	116.5	TEGU_EHV1B	1	P28955	equine herp
1094	5374	5.3	116.5	Q99ND0_MOUSE	2	Q99nd0	mus musculu
1095	5644	5.3	116.5	Q16KQ9_AEDAE	2	Q16kq9	aedes aegyp
1096	168	5.2	116	Q41071_PINTA	2	Q41071	pinus taeda
1097	241	5.2	116	Q38WG5_LACSS	2	Q38wg5	lactobacill
1098	272	5.2	116	Q1XBT3_BHV4	2	Q1xbt3	bovine herp
1099	288	5.2	116	Q4YH55_PLABE	2	Q4yh55	plasmodium
1100	347	5.2	116	Q8SYW5_DROME	2	Q8syw5	drosophila
1101	368	5.2	116	YBX5_SCHPO	1	O10203	schizosacch
1102	488	5.2	116	Q3GTH4_9ACTO	2	Q3gth4	nocardioide
1103	580	5.2	116	Q80X37_MOUSE	2	Q80x37	mus musculu
1104	595	5.2	116	Q4V805_XENLA	2	Q4v805	xenopus lae
1105	622	5.2	116	Q28YV5_DROPS	2	Q28yv5	drosophila
1106	624	5.2	116	YH19_YEAST	1	P38900	saccharomyc
1107	624	5.2	116	Q54MX9_DICDI	2	Q54mx9	dictyosteli
1108	670	5.2	116	YFGG_SCHPO	1	O13854	schizosacch
1109	695	5.2	116	RGA7_SCHPO	1	O94466	schizosacch
1110	722	5.2	116	Q9XTS1_CAEEL	2	Q9xts1	caenorhabdi
1111	730	5.2	116	Q9VNL6_DROME	2	Q9vnl6	drosophila
1112	748	5.2	116	Q6ABW5_LEIXX	2	Q6abw5	leifsonia x
1113	765	5.2	116	Q54PZ3_DICDI	2	Q54pz3	dictyosteli
1114	877	5.2	116	WEE1_SCHPO	1	P07527	schizosacch
1115	877	5.2	116	Q9H3Q6_HUMAN	2	Q9h3q6	homo sapien
1116	906	5.2	116	Q6C951_YARLI	2	Q6c951	yarrowia li
1117	921	5.2	116	Q554C0_DICDI	2	Q554c0	dictyosteli
1118	921	5.2	116	Q869X3_DICDI	2	Q869x3	dictyosteli
1119	925	5.2	116	Q54X70_DICDI	2	Q54x70	dictyosteli
1120	926	5.2	116	AMOT_MOUSE	1	Q8vhg2	mus musculu
1121	954	5.2	116	Q7RZD3_NEUCR	2	Q7rzd3	neurospora
1122	985	5.2	116	Q67643_9ALPH	1	Q67643	gallid herp
1123	1038	5.2	116	Q22RC5_TETTH	2	Q22rc5	tetrahymena
1124	1067	5.2	116	Q5KBA7_CRYNE	2	Q5kba7	cryptococcu
1125	1091	5.2	116	Q4Q6D8_LEIMA	2	Q4q6d8	leishmania
1126	1114	5.2	116	Q7SHB1_NEUCR	2	Q7shb1	neurospora

Seq	Thr	Score	Name	N	Len	Species	Accession
1127	5.2	116	Q5CIS2_CRYHO	2	1126	cryptospori	Q5cis2
1128	5.2	116	Q72WT6_DESVH	2	1131	desulfovibr	Q72wt6
1129	5.2	116	E75BC_DROME	1	1199	drosophila	P17671
1130	5.2	116	PO121_RAT	2	1199	rattus norv	P52591
1131	5.2	116	Q23IY3_TETTH	1	1214	tetrahymena	Q23iy3
1132	5.2	116	CTND2_MOUSE	1	1247	mus musculu	O35927
1133	5.2	116	E75BA_DROME	2	1355	drosophila	P17672
1134	5.2	116	Q16R12_AEDAE	2	1357	aedes aegyp	Q16r12
1135	5.2	116	E75BB_DROME	1	1412	drosophila	P13055
1136	5.2	115.5	Q36FM7_9GAMM	2	1418	shewanella	Q36fm7
1137	5.2	115.5	Q28Z38_DROPS	2	1488	drosophila	Q28z38
1138	5.2	115.5	Q1BUU2_9BURK	2	1527	burkholderi	Q1buu2
1139	5.2	115.5	Q4FX65_LEIMA	2	1677	leishmania	Q4fx65
1140	5.2	116	Q16GJ0_AEDAE	2	2055	aedes aegyp	Q16gj0
1141	5.2	115.5	Q59E65_DROME	2	4129	drosophila	Q59e65
1142	5.2	115.5	Q6RYU7_9MONO	2	236	human metap	Q6ryu7
1143	5.2	115.5	Q5TR24_ANOGA	2	278	anopheles g	Q5tr24
1144	5.2	115.5	MMP3_MYCBO	2	299	mycobacteri	P65379
1145	5.2	115.5	MMP3_MYCTU	2	299	mycobacteri	P65378
1146	5.2	115.5	FIRA_PLAFF	2	310	plasmodium	P06916
1147	5.2	115.5	Q6W762_HUMAN	2	336	homo sapien	Q6w762
1148	5.2	115.5	Q5BKX3_BRARE	2	355	brachydanio	Q5bkx3
1149	5.2	115.5	Q1J828_STRPF	2	393	streptococc	Q1j828
1150	5.2	115.5	Q55PI6_CRYNE	2	447	cryptococcu	Q55pi6
1151	5.2	115.5	Q5ACD4_CANAL	2	463	candida alb	Q5acd4
1152	5.2	115.5	Q8FRY2_COREF	2	486	corynebacte	Q8fry2
1153	5.2	115.5	Q50Q43_ENTHI	2	493	entamoeba h	Q50q43
1154	5.2	115.5	Q6DRJ1_BRARE	2	515	brachydanio	Q6drj1
1155	5.2	115.5	Q84DU3_LISSE	2	516	listeria se	Q84du3
1156	5.2	115.5	Q7S9R3_NEUCR	2	517	neurospora	Q7s9r3
1157	5.2	115.5	TM108_MOUSE	1	574	mus musculu	Q8bhe4
1158	5.2	115.5	Q7O2A5_MYCBO	2	620	mycobacteri	Q7o2a5
1159	5.2	115.5	Q19240_CAEEL	2	625	caenorhabdi	Q19240
1160	5.2	115.5	O77133_CAEEL	2	639	caenorhabdi	O77133
1161	5.2	115.5	Q9SQM5_CAEEL	2	639	caenorhabdi	Q9sqm5
1162	5.2	115.5	Q4N578_THEPA	2	640	theileria p	Q4n578
1163	5.2	115.5	Q9U290_CAEEL	2	675	caenorhabdi	Q9u290
1164	5.2	115.5	Q4QDK4_LEIMA	2	754	leishmania	Q4qdk4
1165	5.2	115.5	CD44_MOUSE	1	778	mus musculu	P15379
1166	5.2	115.5	Q9U3P1_CAEEL	2	952	caenorhabdi	Q9u3p1
1167	5.2	115.5	Q75LK3_ASHGO	2	970	ashbya goss	Q75lk3
1168	5.2	115.5	Q38WH1_LACSS	2	1055	lactobacill	Q38wh1
1169	5.2	115.5	Q9FIY4_ARATH	2	1063	arabidopsis	Q9fiy4
1170	5.2	115.5	MDC1_RAT	1	1279	rattus norv	Q5u2m8
1171	5.2	115.5	Q29DR0_DROPS	2	1491	drosophila	Q29dr0
1172	5.2	115.5	LEUK_HUMAN	1	2483	homo sapien	P16150
1173	5.2	115.5	Q9SVT7_ARATH	2	3402	arabidopsis	Q9svt7
1174	5.2	115	O42665_SCHPO	2	231	schizosacch	O42665
1175	5.2	115	Q66K43_HUMAN	2	326	homo sapien	Q66k43
1176	5.2	115	Q9S7V5_ARATH	2	328	arabidopsis	Q9s7v5
1177	5.2	115	Q4PAU6_USTMA	2	349	ustilago ma	Q4pau6
1178	5.2	115	Q9U6R7_DERFA	2	386	dermatophag	Q9u6r7
1179	5.2	115	Q4IL56_GIBZE	2	400	gibberella	Q4il56
1180	5.2	115	Q7SB86_NEUCR	2	419	neurospora	Q7sb86
1181	5.2	115	Q4I8U1_GIBZE	2	463	gibberella	Q4i8u1
1182	5.2	115	Q8ZD67_YERPE	2	466	yersinia pe	Q8zd67
1183	5.2	115	Q7SG30_NEUCR	2	480	neurospora	Q7sg30
1184	5.2	115	Q668S8_YERPS	2	541	yersinia ps	Q668s8
1185	5.2	115	Q6A036_MOUSE	2	545	mus musculu	Q6a036
1194	5.2	115	Q3TRU9_MOUSE	2	1050	m 12 days e	Q3tru9
1195	5.2	115	Q80TA5_MOUSE	2	1060	mus musculu	Q80ta5
1196	5.2	115	Q55MX7_CRYNE	2	1067	cryptococcu	Q55mx7
1197	5.2	115	Q4IHX0_GIBZE	2	1184	gibberella	Q4ihx0
1198	5.2	115	Q4WKG6_ASPFU	2	1258	aspergillus	Q4wkg6
1199	5.2	115	Q16TD7_AEDAE	2	1309	aedes aegyp	Q16td7

Seq	Thr	Score	Len	N	Name	Accession	Species
1200	5.2	115	1324	2	Q2M0D0_DROPS	Q2m0d0	drosophila
1201	5.2	115	1370	2	Q8BZ32_MOUSE	Q8bz32	mus musculu
1202	5.2	115	1425	2	Q86CW3_DROSE	Q86cw3	drosophila
1203	5.2	115	1457	2	Q6IRM3_XENLA	Q6irm3	xenopus lae
1204	5.2	115	1763	2	Q4HX73_GIBZE	Q4hx73	gibberella
1205	5.2	115	2125	2	Q55EJ1_DICDI	Q55ej1	dictyosteli
1206	5.2	115	2152	2	Q5TQQ3_ANOGA	Q5tqq3	anopheles g
1207	5.2	115	2548	2	Q9WRN0_9GAMA	Q9wrn0	macaca mula
1208	5.2	115	2548	2	Q9J2I8_9GAMA	Q9j2i8	rhesus monk
1209	5.2	114.5	289	2	Q2LZ60_DROPS	Q2lz60	drosophila
1210	5.2	114.5	362	2	Q4X837_PLACH	Q4x837	plasmodium
1211	5.2	114.5	364	2	Q9W2Z7_DROME	Q9w2z7	drosophila
1212	5.2	114.5	384	2	Q30BZ1_9STRA	Q30bz1	phytophthor
1213	5.2	114.5	472	2	Q54KV7_DICDI	Q54kv7	dictyosteli
1214	5.2	114.5	475	2	Q8FQJ1_COREF	Q8fqj1	corynebacte
1215	5.2	114.5	495	2	Q29KR2_DROPS	Q29kr2	drosophila
1216	5.2	114.5	514	2	Q9NWD4_HUMAN	Q9nwd4	homo sapien
1217	5.2	114.5	619	2	Q55A39_DICDI	Q55a39	dictyosteli
1218	5.2	114.5	620	2	Q9AV95_SOYBN	Q9av95	glycine max
1219	5.2	114.5	653	2	Q5WRN8_CAEEL	Q5wrn8	caenorhabdi
1220	5.2	114.5	693	2	Q07241_PNECA	Q07241	pneumocysti
1221	5.2	114.5	721	2	Q5B8P4_EMENI	Q5b8p4	emericella
1222	5.2	114.5	810	2	Q4IS00_GIBZE	Q4is00	gibberella
1223	5.2	114.5	812	2	Q6BJD1_DEBHA	Q6bjd1	debaryomyce
1224	5.2	114.5	817	2	Q6PGX9_BRARE	Q6pgx9	brachydanio
1225	5.2	114.5	902	2	Q4RJ31_TETNG	Q4rj31	tetraodon n
1226	5.2	114.5	919	2	Q6G217_BARHE	Q6g217	bartonella
1227	5.2	114.5	922	2	Q6FK94_CANGA	Q6fk94	candida gla
1228	5.2	114.5	945	2	Q9YGM0_CHICK	Q9ygm0	gallus gall
1229	5.2	114.5	981	2	Q6PFI6_BRARE	Q6pfi6	brachydanio
1230	5.2	114.5	991	2	Q6UDF7_9ALPH	Q6udf7	psittacid h
1231	5.2	114.5	993	2	Q7S6Z8_NEUCR	Q7s6z8	neurospora
1232	5.2	114.5	1096	2	Q1SM92_MEDTR	Q1sm92	medicago tr
1233	5.2	114.5	1100	2	O57576_CYNPY	O57576	cynops pyrr
1234	5.2	114.5	1217	2	P91457_CAEEL	P91457	caenorhabdi
1235	5.2	114.5	1313	2	Q80WC1_MOUSE	Q80wc1	mus musculu
1236	5.2	114.5	1354	2	Q4N958_THEPA	Q4n958	theileria p
1237	5.2	114.5	1435	2	Q4FX64_LEIMA	Q4fx64	leishmania
1238	5.2	114.5	1523	2	Q4FPJ7_PELUB	Q4fpj7	pelagibacte
1239	5.2	114.5	1571	2	Q1V0H5_9RICK	Q1v0h5	candidatus
1240	5.2	114.5	1576	2	Q9I908_XENLA	Q9i908	xenopus lae
1241	5.2	114.5	1701	2	Q7KTF6_DROME	Q7ktf6	drosophila
1242	5.2	114.5	1736	2	Q54DW1_DICDI	Q54dw1	dictyosteli
1243	5.2	114.5	2520	2	Q4MNM6_BACCE	Q4mnm6	bacillus ce
1244	5.2	114.5	2520	2	Q6HFE0_BACHK	Q6hfe0	bacillus th
1245	5.2	114.5	9606	2	Q4ABG9_DROME	Q4abg9	drosophila
1246	5.2	114	215	2	Q4DCE6_TRYCR	Q4dce6	trypanosoma
1247	5.2	114	247	2	Q8MKY7_DROME	Q8mky7	drosophila
1248	5.2	114	260	2	Q8V0K6_9ALPH	Q8v0k6	equid herpe
1249	5.2	114	276	2	Q2N093_9STRA	Q2n093	phytophthor
1250	5.2	114	289	2	Q2QSL3_ORYSA	Q2qsl3	oryza sativ
1251	5.2	114	293	2	Q9CCE9_MYCLE	Q9cce9	mycobacteri
1252	5.2	114	310	2	Q16RY7_AEDAE	Q16ry7	aedes aegyp
1253	5.2	114	358	2	Q8FQU1_COREF	Q8fqu1	corynebacte
1254	5.2	114	368	2	Q1TCS5_9MYCO	Q1tcs5	mycobacteri
1255	5.2	114	368	2	Q1BCV7_9MYCO	Q1bcv7	mycobacteri
1256	5.2	114	386	2	Q4CZ98_TRYCR	Q4cz98	trypanosoma
1257	5.2	114	387	2	Q4D265_TRYCR	Q4d265	trypanosoma
1258	5.2	114	389	2	Q263T6_MYCVN	Q263t6	mycobacteri
1259	5.2	114	396	2	Q1GRV5_9SPHN	Q1grv5	sphingopyxi
1260	5.2	114	442	1	SDC3_RAT	P33671	rattus norv
1261	5.2	114	479	2	Q2TZZ8_ASPOR	Q2tzz8	aspergillus
1262	5.2	114	507	1	CRH1_YEAST	P53301	saccharomyc
1263	5.2	114	510	2	O04210_ARATH	O04210	arabidopsis
1264	5.2	114	516	2	Q54Z21_DICDI	Q54z21	dictyosteli
1265	5.2	114	523	2	Q84DM1_LISSE	Q84dm1	listeria se
1266	5.2	114	566	1	P60_LISSE	Q01838	listeria se
1267	5.2	114	566	2	Q1E858_COCIM	Q1e858	coccidioide
1268	5.2	114	581	2	Q55EK7_DICDI	Q55ek7	dictyosteli
1269	5.2	114	583	2	Q2GQX8_CHAGB	Q2gqx8	chaetonium
1270	5.2	114	589	2	Q4SN49_TETNG	Q4sn49	tetraodon n
1271	5.2	114	607	2	Q494P4_ARATH	Q494p4	arabidopsis
1272	5.2	114	617	2	Q16PE7_ABDAE	Q16pe7	aedes aegyp

1273	114	5.2	625	Q6CAK4_YARLI	2	yarrowia li
1274	114	5.2	626	Q9NDD1_LEITR	2	leishmania
1275	114	5.2	655	FOXK2_HUMAN	1	homo sapien
1276	114	5.2	682	Q9AVE4_PEA	2	pisum sativ
1277	114	5.2	753	Q5AEG7_CANAL	2	candida alb
1278	114	5.2	767	Q1UBY7_9GAMM	2	psychrobact
1279	114	5.2	807	Q4Q0Y9_LEIMA	2	leishmania
1280	114	5.2	819	Q30926_9RODE	2	eospalax ba
1281	114	5.2	838	Q60VT0_CAEBR	2	caenorhabdi
1282	114	5.2	879	Q4IC17_GIBZE	2	gibberella
1283	114	5.2	883	Q17JB9_AEDAE	2	aedes aegyp
1284	114	5.2	892	Q4DQ76_TRYCR	2	trypanosoma
1285	114	5.2	918	Q7Q3F0_ANOGA	2	anopheles g
1286	114	5.2	1013	Q9X233_DROME	2	drosophila
1287	114	5.2	1015	Q8SZW9_DROME	2	drosophila
1288	114	5.2	1105	Q7YU57_DROME	2	drosophila
1289	114	5.2	1192	Q8ISS2_PLUXY	2	plutella xy
1290	114	5.2	1220	Q4HYG4_GIBZE	2	gibberella
1291	114	5.2	1225	Q4I752_GIBZE	2	gibberella
1292	114	5.2	1269	Q54CA1_DICDI	2	dictyosteli
1293	114	5.2	1292	Q9LPN4_ARATH	2	arabidopsis
1294	114	5.2	1305	Q1RPV8_CIOIN	2	ciona intes
1295	114	5.2	1309	Q9CAF4_ARATH	2	arabidopsis
1296	114	5.2	1332	Q6ZPI6_MOUSE	2	mus musculu
1297	114	5.2	1348	Q86KE2_DICDI	2	dictyosteli
1298	114	5.2	1349	Q6PAN9_MOUSE	2	mus musculu
1299	114	5.2	1405	Q86CW4_DROSI	2	drosophila
1300	114	5.2	1413	Q86CV8_DROME	2	drosophila
1301	114	5.2	1413	Q86CV9_DROME	2	drosophila
1302	114	5.2	1413	Q86CW1_DROME	2	drosophila
1303	114	5.2	1413	Q86CW5_DROME	2	drosophila
1304	114	5.2	1415	Q6CHK3_YARLI	2	yarrowia li
1305	114	5.2	1422	Q2H171_CHAGB	2	chaetomium
1306	114	5.2	1424	Q5K868_CRYNE	2	cryptococcu
1307	114	5.2	1472	Q61YT8_CAEBR	2	caenorhabdi
1308	114	5.2	1486	Q55410_DICDI	2	dictyosteli
1309	114	5.2	1547	Q26471_SCHAM	2	schistocerc
1310	113.5	5.1	1557	Q81IF2_MOUSE	2	mus musculu
1311	113.5	5.1	2065	Q3UH66_MOUSE	2	mus musculu
1312	113.5	5.1	2082	Q7PQ78_ANOGA	2	anopheles g
1313	113.5	5.1	2173	MDC1_MACMU	1	macaca mula
1314	113.5	5.1	2486	Q9VXM5_DROME	2	drosophila
1315	113.5	5.1	2781	Q9UIG2_HUMAN	2	homo sapien
1316	113.5	5.1	3300	Q4N127_THEPA	2	theileria p
1317	113.5	5.1	4582	Q54T85_DICDI	2	dictyosteli
1318	113.5	5.1	143	O15776_TRYCR	2	trypanosoma
1319	113.5	5.1	223	Q7TFI9_RHCM6	2	rhesus cyto
1320	113.5	5.1	232	Q7D9P2_DROME	2	drosophila
1321	113.5	5.1	236	Q4V322_DROME	2	drosophila
1322	113.5	5.1	295	Q32850_MYCBO	2	mycobacteri
1323	113.5	5.1	354	Q61916_MOUSE	2	mus musculu
1324	113.5	5.1	373	YLU2_PICAN	2	pichia angu
1325	113.5	5.1	411	Q702X9_HHV1	2	human herpe
1326	113.5	5.1	542	POL5_MOUSE	1	mus musculu
1327	113.5	5.1	543	EGR1_HUMAN	1	homo sapien
1328	113.5	5.1	543	Q54G51_HUMAN	2	homo sapien
1329	113.5	5.1	548	Q7D9P2_MYCTU	2	mycobacteri
1330	113.5	5.1	548	O06404_MYCTU	2	mycobacteri
1331	113.5	5.1	548	Q7UIT8_MYCBO	2	mycobacteri
1332	113.5	5.1	554	Q17KK2_AEDAE	2	aedes aegyp
1333	113.5	5.1	627	Q9XW47_CAEEL	2	caenorhabdi
1334	113.5	5.1	637	Q6BNH4_DEBHA	2	debaryomyce
1335	113.5	5.1	668	Q6FWR2_CANGA	2	candida gla
1336	113.5	5.1	703	Q6BXK5_DEBHA	2	debaryomyce
1337	113.5	5.1	710	Q5M259_STRT2	2	streptococc
1338	113.5	5.1	738	Q4A3Y3_RUMFL	2	ruminococcu
1339	113.5	5.1	748	Q16I33_AEDAE	2	aedes aegyp
1340	113.5	5.1	789	Q5LXK8_STRT1	2	streptococc
1341	113.5	5.1	808	Q69L88_ORYSA	2	oryza sativ
1342	113.5	5.1	814	Q3E132_CHLAU	2	chloroflexu
1343	113.5	5.1	843	Q29197_DROPS	2	drosophila
1344	113.5	5.1	851	Q9QP86_EBVG	2	epstein-bar
1345	113.5	5.1	890	Q5ZLP9_CHICK	2	gallus gall

1346	113.5	5.1	906	Q4P347_USTMA	2	ustilago ma
1347	113.5	5.1	913	Q5F3A3_CHICK	2	gallus gall
1348	113.5	5.1	915	Q4FZU8_RAT	2	rattus norv
1349	113.5	5.1	987	Q4SYG9_TETNG	2	tetraodon n
1350	113.5	5.1	1086	Q59XL0_CANAL	2	candida alb
1351	113.5	5.1	1167	Q7RWQ7_NEUCR	2	neurospora
1352	113.5	5.1	1286	Q9VR49_DROME	2	drosophila
1353	113.5	5.1	1359	Q9NF31_DROME	2	drosophila
1354	113.5	5.1	1533	Q2HGL9_CHAGB	2	chaetomium
1355	113.5	5.1	1537	Q9W523_DROME	2	drosophila
1356	113.5	5.1	1562	Q16WL5_AEDAE	2	aedes aegyp
1357	113.5	5.1	1727	Q68FD9_MOUSE	2	mus musculu
1358	113.5	5.1	2063	Q86B73_DROME	2	drosophila
1359	113.5	5.1	2171	MDC1_PANTR	1	pan troglod
1360	113.5	5.1	2520	Q637G8_BACCZ	2	bacillus ce
1361	113.5	5.1	4106	Q8XQP2_RALSO	2	ralstonia s
1362	113.5	5.1	5017	Q81SN0_BACAN	2	bacillus an
1363	113	5.1	128	Q4CVG2_TRYCR	2	trypanosoma
1364	113	5.1	220	Q9EQG0_MOUSE	2	mus musculu
1365	113	5.1	259	Q2KG75_MAGGR	2	magnaporthe
1366	113	5.1	307	SGS3_DROME	1	drosophila
1367	113	5.1	349	Q6P0S4_BRARE	2	brachydanio
1368	113	5.1	442	Q7TQD4_MOUSE	2	mus musculu
1369	113	5.1	482	Q6UX97_HUMAN	2	homo sapien
1370	113	5.1	486	Q6ZQA4_MOUSE	2	mus musculu
1371	113	5.1	489	Q60SR0_CAEBR	2	caenorhabdi
1372	113	5.1	496	Q88VA6_LACPL	2	lactobacill
1373	113	5.1	503	Q76185_HUMAN	2	homo sapien
1374	113	5.1	522	NUP62_HUMAN	1	homo sapien
1375	113	5.1	522	Q6GTM2_HUMAN	2	homo sapien
1376	113	5.1	538	Q86ST8_HUMAN	2	homo sapien
1377	113	5.1	541	Q3U7R5_MOUSE	2	mus musculu
1378	113	5.1	550	Q4I9I4_GIBZE	2	gibberella
1379	113	5.1	582	Q59SC9_CANAL	2	candida alb
1380	113	5.1	595	HSV2_CANAL	1	candida alb
1381	113	5.1	616	Q58EE4_BRARE	2	brachydanio
1382	113	5.1	714	Q6DTM6_CANGA	2	candida gla
1383	113	5.1	751	Q1DLZ8_COCIM	2	coccidioide
1384	113	5.1	760	Q54P01_DICDI	2	dictyosteli
1385	113	5.1	773	Q398E2_BURS3	2	burkholderi
1386	113	5.1	789	Q5RCI8_PONPY	2	pongo pygma
1387	113	5.1	814	Q55AJ1_DICDI	2	dictyosteli
1388	113	5.1	877	Q55CK2_DICDI	2	dictyosteli
1389	113	5.1	906	Q54MV3_DICDI	2	dictyosteli
1390	113	5.1	912	Q960V1_DROME	2	drosophila
1391	113	5.1	916	Q9VTB1_DROME	2	drosophila
1392	113	5.1	931	Q59LQ1_CANAL	2	candida alb
1393	113	5.1	933	Q55F35_DICDI	2	dictyosteli
1394	113	5.1	943	Q7S322_NEUCR	2	neurospora
1395	113	5.1	955	Q2XXX4_DROYA	2	drosophila
1396	113	5.1	984	Q96HA1_HUMAN	2	homo sapien
1397	113	5.1	1053	Q2H4U4_CHAGB	2	chaetomium
1398	113	5.1	1062	Q5TSX6_ANOGA	2	anopheles g
1399	113	5.1	1114	Q6P9L3_MOUSE	2	mus musculu
1400	113	5.1	1115	Q4RRV4_TETNG	2	tetraodon n
1401	113	5.1	1117	Q4I445_GIBZE	2	gibberella
1402	113	5.1	1187	Q7PZE7_ANOGA	2	anopheles g
1403	113	5.1	1293	Q1D082_MYXXA	2	myxococcus
1404	113	5.1	1297	Q8SSS5_DICDI	2	dictyosteli
1405	113	5.1	1365	Q55AD5_DICDI	2	dictyosteli
1406	113	5.1	1519	Q7Z3C4_HUMAN	2	homo sapien
1407	113	5.1	1537	FLO1_YEAST	1	saccharomyc
1408	113	5.1	1537	Q58HH7_YEAST	2	saccharomyc
1409	113	5.1	1592	Q5AWR8_EMENI	2	emericella
1410	113	5.1	1684	Q5JUP9_HUMAN	2	homo sapien
1411	113	5.1	1798	Q16FJ6_AEDAE	2	aedes aegyp
1412	113	5.1	2080	Q3KQZ0_HUMAN	2	homo sapien
1413	113	5.1	2090	NU214_HUMAN	1	homo sapien
1414	113	5.1	2090	Q86XD3_HUMAN	2	homo sapien
1415	113	5.1	2090	Q5JUP7_HUMAN	2	homo sapien
1416	113	5.1	2091	Q75R47_HUMAN	2	homo sapien
1417	113	5.1	2093	Q15010_HUMAN	2	homo sapien
1418	113	5.1	2425	Q4FX61_LEIMA	2	leishmania

1419	113	5.1	Q9VPI3_DROME	Q9VPI3 drosophila
1420	113	5.1	Q4L9P0_STAHJ	Q4L9P0 staphylococc
1421	112.5	5.1	Q9U9J1_TOXCA	Q9U9J1 toxocara ca
1422	112.5	5.1	Q8J1N6_SACPA	Q8J1N6 saccharomyc
1423	112.5	5.1	Q73YL7_MYCPA	Q73YL7 mycobacteri
1424	112.5	5.1	Q83ND0_TROW8	Q83ND0 tropheryma
1425	112.5	5.1	TIMD4_HUMAN	Q96H15 homo sapien
1426	112.5	5.1	Q54KW2_DICDI	Q54KW2 dictyosteli
1427	112.5	5.1	Q16Q12_AEDAE	Q16Q12 aedes aegyp
1428	112.5	5.1	Q30BY3_9STRA	Q30BY3 phytophthor
1429	112.5	5.1	Q5M6K4_STRT2	Q5M6K4 streptococc
1430	112.5	5.1	Q6A044_MOUSB	Q6A044 mus musculu
1431	112.5	5.1	Q6CCG0_YARLI	Q6CCG0 yarrowia li
1432	112.5	5.1	Q4IQU7_GIBZE	Q4IQU7 gibberella
1433	112.5	5.1	Q4WY55_ASPFU	Q4WY55 aspergillus
1434	112.5	5.1	O19115_RABIT	O19115 oryctolagus
1435	112.5	5.1	AL2S8_MOUSE	Q8VHi4 mus musculu
1436	112.5	5.1	Q53N6_HUMAN	Q53N6 homo sapien
1437	112.5	5.1	Q4IN81_GIBZE	Q4IN81 gibberella
1438	112.5	5.1	Q2UPS1_ASPOR	Q2UPS1 aspergillus
1439	112.5	5.1	Q5NRN7_SOLDE	Q5NRN7 solanum dem
1440	112.5	5.1	Q6C9X3_YARLI	Q6C9X3 yarrowia li
1441	112.5	5.1	Q5CW90_CRYPV	Q5CW90 cryptospori
1442	112.5	5.1	EPC2_HUMAN	Q52LR7 homo sapien
1443	112.5	5.1	Q2M124_DROPS	Q2M124 drosophila
1444	112.5	5.1	Q8SWW5_DROME	Q8SWW5 drosophila
1445	112.5	5.1	Q6FVN2_CANGA	Q6FVN2 candida gla
1446	112.5	5.1	Q9SU80_DROME	Q9SU80 drosophila
1447	112.5	5.1	Q9VF64_DROME	Q9VF64 drosophila
1448	112.5	5.1	Q8IHA4_DROME	Q8IHA4 drosophila
1449	112.5	5.1	Q8X0X1_NEUCR	Q8X0X1 neurospora
1450	112.5	5.1	PHC3_HUMAN	Q8NDX5 homo sapien
1451	112.5	5.1	Q8INE0_DROME	Q8INE0 drosophila
1452	112.5	5.1	Q8IS18_DICDI	Q8IS18 dictyosteli
1453	112.5	5.1	Q55CK1_DICDI	Q55CK1 dictyosteli
1454	112.5	5.1	Q4BKU3_BURVI	Q4BKU3 burkholderi
1455	112.5	5.1	Q9W294_DROME	Q9W294 drosophila
1456	112.5	5.1	Q9CF64_LACLA	Q9CF64 lactococcus
1457	112.5	5.1	Q8SWR8_DROME	Q8SWR8 drosophila
1458	112.5	5.1	Q1DZI1_COCIM	Q1DZI1 coccidioide
1459	112.5	5.1	Q54DZ1_DICDI	Q54DZ1 dictyosteli
1460	112.5	5.1	Q7WYN2_9CLOT	Q7WYN2 acetivibrio
1461	112.5	5.1	Q29E98_DROPS	Q29E98 drosophila
1462	112.5	5.1	Q4IQ3_GIBZE	Q4I2Q3 gibberella
1463	112.5	5.1	Q96TY0_NEUCR	Q96TY0 neurospora
1464	112.5	5.1	Q7S7T0_NEUCR	Q7S7T0 neurospora
1465	112.5	5.1	Q9V9S7_DROME	Q9V9S7 drosophila
1466	112.5	5.1	Q91909_XENLA	Q91909 xenopus lae
1467	112.5	5.1	Q4Q3P5_LEIMA	Q4Q3P5 leishmania
1468	112.5	5.1	Q6HKW5_BACHK	Q6HKW5 bacillus th
1469	112	5.1	Q4WAA2_ASPFU	Q4WAA2 aspergillus
1470	112	5.1	Q17260_BRUPA	Q17260 brugia paha
1471	112	5.1	Q90146_9BETA	Q90146 macaca mula
1472	112	5.1	Q1ECV7_BRARE	Q1ECV7 brachydanio
1473	112	5.1	Q1F9H1_9CHLR	Q1F9H1 roseiflexus
1474	112	5.1	Q6W763_HUMAN	Q6W763 homo sapien
1475	112	5.1	Q26596_SCHMA	Q26596 schistosoma
1476	112	5.1	Q4CKY7_TRYCR	Q4CKY7 trypanosoma
1477	112	5.1	Q753G3_ASHGO	Q753G3 ashbya goss
1478	112	5.1	Q7R6A7_GIALA	Q7R6A7 giardia lam
1479	112	5.1	Q5AFT5_CANAL	Q5AFT5 candida alb
1480	112	5.1	Q6FSM3_CANGA	Q6FSM3 candida gla
1481	112	5.1	Q4YZB1_PLABE	Q4YZB1 plasmodium
1482	112	5.1	Q3TEI6_MOUSE	Q3TEI6 m 2 days ne
1483	112	5.1	Q8WTT8_HUMAN	Q8WTT8 homo sapien
1484	112	5.1	Q9BQC9_HUMAN	Q9BQC9 homo sapien
1485	112	5.1	Q8CAR4_MOUSE	Q8CAR4 mus musculu
1486	112	5.1	Q7T363_BRARE	Q7T363 brachydanio
1487	112	5.1	Q4I9S2_GIBZE	Q4I9S2 gibberella
1488	112	5.1	Q29MV7_DROPS	Q29MV7 drosophila
1489	112	5.1	Q55J23_CRYNE	Q55J23 cryptococcu
1490	112	5.1	Q8PWB3_METMA	Q8PWB3 methanosarc
1491	112	5.1	Q4WJC3_ASPFU	Q4WJC3 aspergillus

1492	112	5.1	Q60W81_CAEBR	Q60w81 caenorhabdi
1493	112	5.1	Q6CF33_YARLI	Q6cf33 yarrowia li
1494	112	5.1	Q4IOH0_GIBZE	Q4io0h gibberella
1495	112	5.1	Q4Q1T0_LEIMA	Q4q1t0 leishmania
1496	112	5.1	Q76I84_MOUSE	Q76i84 mus musculu
1497	112	5.1	Q5B5D4_EMENI	Q5b5d4 emericella
1498	112	5.1	Q17J55_AEDAE	Q17j55 aedes aegyp
1499	112	5.1	Q80UR5_MOUSE	Q80ur5 mus musculu
1500	112	5.1	Q9DES7_BRARE	Q9des7 brachydanio

ALIGNMENTS

RESULT 1
MANS1_HUMAN
ID   MANS1_HUMAN   STANDARD;   PRT;   431 AA.
AC   Q9H8J5; Q8NEC1;
DT   07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT   01-MAR-2001, sequence version 1.
DT   11-JUL-2006, entry version 28.
DE   MANSC domain-containing protein 1 precursor.
GN   Name=MANSC1; ORFNames=UNQ316/PRO361;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Placenta;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA   Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA   Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA   Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA   Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

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RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ILE-55.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Contains 1 MANSC domain.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK023622; BAB14621.1; -; mRNA.
DR   EMBL; AY358563; AAQ88926.1; -; mRNA.
DR   EMBL; BC032998; AAH32998.1; -; mRNA.
DR   UniGene; Hs.591145; -.
DR   Ensembl; ENSG00000111261; Homo sapiens.
DR   HGNC; HGNC:25505; MANSC1.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANEC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Glycoprotein; Membrane; Polymorphism; Signal; Transmembrane.
FT   SIGNAL          1     26       Potential.
FT   CHAIN          27    431       MANSC domain-containing protein 1.
FT                                  /FTId=PRO_0000021636.
FT   TOPO_DOM       27    385       Extracellular (Potential).
FT   TRANSMEM      386    408       Potential.
FT   TOPO_DOM      409    431       Cytoplasmic (Potential).
FT   DOMAIN         33    117       MANSC.
FT   COMPBIAS      237    332       Thr-rich.
FT   CARBOHYD       72     72       N-linked (GlcNAc...)    (Potential).
FT   CARBOHYD      222    222       N-linked (GlcNAc...)    (Potential).
FT   CARBOHYD      251    251       N-linked (GlcNAc...)    (Potential).
FT   CARBOHYD      327    327       N-linked (GlcNAc...)    (Potential).
FT   CARBOHYD      352    352       N-linked (GlcNAc...)    (Potential).
FT   VARIANT        55     55       V -> I (in dbSNP:3741799).
FT                                  /FTId=VAR_021840.
FT   VARIANT       375    375       N -> Y (in dbSNP:3741803).
FT                                  /FTId=VAR_021841.
SQ   SEQUENCE   431 AA;  46810 MW;  18913641 6F0F89AE CRC64;

Query Match             100.0%;  Score 2211;  DB 1;  Length 431;
Best Local Similarity   100.0%;  Pred. No. 8.5e-137;
Matches   431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1  MFFGGEGSLYTLVIICFLTLRLSASONCLKKSLEDVVIDIQSLSKGIRGNEPVYTSTQ  60
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Db    1  MFFGGEGSLYTLVIICFLTLRLSASONCLKKSLEDVVIDIQSLSKGIRGNEPVYTSTQ  60

Qy   61  EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120
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Db   61  EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120

Qy  121  TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD  180
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Db  121  TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD  180

Qy  181  HLEKLFKMDRASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA  240
         |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA  240

Qy  241  TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT  300
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Db  241  TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT  300

Qy  301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR  360
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Db  301  AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR  360

Qy  361  EASPGSSSQGSVPENOYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420
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Db  361  EASPGSSSQGSVPENOYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420

Qy  421  DYLINGIYVDI  431
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Db  421  DYLINGIYVDI  431


RESULT 2
Q5RAU3_PONPY
ID   Q5RAU3_PONPY            PRELIMINARY;      PRT;    431 AA.
AC   Q5RAU3;
DT   21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   21-DEC-2004, sequence version 1.
DT   30-MAY-2006, entry version 5.
DE   Hypothetical protein DKFZp469A172.
GN   Name=DKFZp469A172;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   The German cDNA Consortium;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CR858919; CAH91117.1; -; mRNA.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANEC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   431 AA;  47007 MW;  81FB90ED5051BACB CRC64;

Query Match             95.5%;  Score 2111;  DB 2;  Length 431;
Best Local Similarity   95.4%;  Pred. No. 3.1e-130;
Matches   411;  Conservative    6;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    1  MFFGGEGSLYTLVIICFLTLRLSASONCLKKSLEDVVIDIQSLSKGIRGNEPIYTSTQ  60
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Db    1  MFFGGEGSLYTLVIICFLTLRLSASQDCLNKSLEDVVIDIQSLSKGIRGNEPIYTSTQ  60

Qy   61  EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120
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Db   61  EDCINSCCSTKNISGDRACNLMIFDTRKTARQPNCYLFFCPDEEACPLRPAKGLMSYRII  120
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SQ   SEQUENCE   431 AA;   47105 MW;   BF10996E87F76C69 CRC64;

     Query Match             92.2%;   Score 2039;   DB 1;   Length 431;
     Best Local Similarity   92.3%;   Pred. No. 1.7e-125;
     Matches 398;   Conservative   9;   Mismatches   24;   Indels   0;   Gaps   0;

Qy      1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLRDVVIDIQSSLSKGIRGNEPVYTSTQ  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MFFGGKGSLTYTLVIICFLTLRLAAASQNCLNKSLEDVVIDIQSSLSKGIRGNEPIYTSTQ  60

Qy     61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII  120
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Qy    121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD  180
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Qy    181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA  240
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Qy    241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TPKPAIRLPTNASVTPSGTSQPQLATTSPPVTVTSQPPTTLISTGFTRAVATLQAMATT  300

Qy    301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AVLTTTFQAPTDLKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVAKSSATNKTASWEGR  360

Qy    361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 EASPGRSSQGNRVPENQYGLPFEKWLLIGSLLFGVLFLVIGLLILLGRILSESLRRKRYSRL  420

Qy    421 DYLINGIYVDI  431
          ||||||||||
Db    421 DYLINGIYVDI  431


RESULT 3
MANS1_MACFA
ID   MANS1_MACFA   STANDARD;   PRT;   431 AA.
AC   Q95KG7;
DT   07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT   01-DEC-2001, sequence version 1.
DT   11-JUL-2006, entry version 26.
DE   MANSC domain-containing protein 1 precursor.
GN   Name=MANSC1; ORFNames=QtrA-13483;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Temporal cortex;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Contains 1 MANSC domain.
CC   ---------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------------
DR   EMBL; AB060888; BAB46892.1; -; mRNA.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANEC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Glycoprotein; Membrane; Signal; Transmembrane.
FT   SIGNAL        1     26       Potential.
FT   CHAIN        27    431       MANSC domain-containing protein 1.
FT                               /FTId=PRO_0000021637.
FT   TOPO_DOM     27    385       Extracellular (Potential).
FT   TRANSMEM    386    408       Potential.
FT   TOPO_DOM    409    431       Cytoplasmic (Potential).
FT   DOMAIN       33    117       MANSC.
FT   COMPBIAS    237    332       Thr-rich.
FT   CARBOHYD     31     31       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    251    251       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    327    327       N-linked (GlcNAc...)   (Potential).
FT   CARBOHYD    352    352       N-linked (GlcNAc...)   (Potential).


RESULT 4
Q9NW60_HUMAN
ID   Q9NW60_HUMAN   PRELIMINARY;   PRT;   397 AA.
AC   Q9NW60;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   13-JUN-2006, entry version 18.
DE   CDNA FLJ10298 fis, clone NT2RM1001115, weakly similar to ENDOCHITINASE
DE   2 (EC 3.2.1.14).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA   Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA   Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA   Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA   Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
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RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Fujiwara A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AK001160; BAA91526.1; -; mRNA.
DR   Ensembl; ENSG00000111261; Homo sapiens.
DR   GO; GO:0004568; F:chitinase activity; IEA.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANEC; 1.
DR   PROSITE; PS50986; MANSC; 1.
SQ   SEQUENCE   397 AA;   43063 MW;   E2FEFF2E61122C62 CRC64;

Query Match             91.5%;  Score 2022;  DB 2;  Length 397;
Best Local Similarity   92.1%;  Pred. No. 2e-124;
Matches  397;  Conservative   0;  Mismatches   0;  Indels  34;  Gaps  1;

Qy          1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSLSKGIRGNEPVYTSTQ 60
              |||||||||||                                       ||||||||||
Db          1 MFFGGEGSLTYTL-------------------------------------GIRGNEPVYTSTQ 26

Qy         61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 86

Qy        121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPFDISWRDTLSQKFGSSD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPFDISWRDTLSQKFGSSD 146

Qy        181 HLEKLFKMDEASAQLLAYKEKGHSQSQSQFSSDQEIAHLLPENVSALPATVAVASPHTSA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 HLEKLFKMDEASAQLLAYKEKGHSQSQSQFSSDQEIAHLLPENVSALPATVAVASPHTSA 206

Qy        241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT 266

Qy        301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 326

Qy        361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 386

Qy        421 DYLINGIYVDI 431
              |||||||||||
Db        387 DYLINGIYVDI 397


RESULT 5
Q3TAH6_MOUSE
ID   Q3TAH6_MOUSE            PRELIMINARY;      PRT;   414 AA.
AC   Q3TAH6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Activated spleen cDNA, RIKEN full-length enriched library,
DE   clone:F830014E01 product:hypothetical Seven cysteines, N-terminal
DE   containing protein, full insert sequence.
GN   Name=Manscl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=22354681; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
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RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420;563-573 (2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409;685-690 (2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=20530911; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka H., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.

RC   STRAIN=NOD; TISSUE=Activated spleen;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H. Nomura K., Ohno H., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK171842; BAB24692.1; -; mRNA.
DR   MGI; MGI:1914979; Mansc1.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANEC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   414 AA; 44547 MW; 6550DA67D0394A70 CRC64;

Query Match   53.2%; Score 1176.5; DB 2; Length 414;
Best Local Similarity   59.9%; Pred. No. 7e-69;
Matches 258; Conservative   39; Mismatches 117; Indels   17; Gaps   6;

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Qy    1 MFFGGGSLYTVLVICFLTRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ  60
          ||  | ::|:||:|| |::|| ||||:|||||||||||::||
Db    1 MLFRGT-SLAYSLLVISFLTPRSSAGQNCLYKSLEDVVIDIQSSLSKGIRGNEPIHVATQ  59

Qy   61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEEACPLKPAKGLMSYRII 120
         ||:|| ||||||:||||||||||||||||:::||:||||||:::||||||||||::|:
Db   60 EDCVGACCSTKDIAGDKACNLMIFDTRKTDRQPNCYLFFCPSEDACPLKPAKGLVTYRLv 119

Qy  121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
         .||| |:||:..| | .|||||..|..|.||.....|..||| ...|.|.|:.||::.|
Db  120 RDFPLTSANSSLQQLTQGESLLLDHSSPGATPGFRTPAGYPKPTGLSWSDGSSLKSTAPL 179

Qy  181 HLEKLFKMDRASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
         ||.|..|.||:..|.....:.:.||||:||.::||:..||||:|.||.|:...||..::.
Db  180 HLRKHIKADETSTQL--PEEKSHSQSLQLPSSLKMAHLLPKTVPTPPTTVAVAPLRNVSA 237

Qy  241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
         | ||| ||.:.:.:.||.|.|| |...||.:|.:.||| |.| ...:.:||:.:....:.
Db  238 TLKPALL-TSISVTAKTLKQKE-ATTASPVTTVTSKLPAVPGSTSFT-----PVVTHQ  289

Qy  301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
         |.|..|||| |||||.|||:|| .. .||.....|.|.|.| ..|:.||:.|:||||||:|
Db  290 AALTNTFQAHTDSKGILETMPFQGGSTLiT------SDPRHGKSSTSESSITNKTASWEDR 343

Qy  361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLGRILSESLRRKRYSRL 420
         ..|| ||:|:...:.|| ||.:.::|||:||.|.||||||||||||::|:|.|||:|||||
Db  344 RVSVGSASLNKGPKSQHGLSPEKWLLIGTLLCGVLFLVIGLVLGRMLVEALRRKRYSRL 403

Qy  421 DYLINGIYVDI 431
         |||||||||||
Db  404 DYLINGIYVDI 414
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RESULT 6
MANS1_MOUSE
ID   MANS1_MOUSE   STANDARD;   PRT;   414 AA.
AC   Q9CR33; Q80V71;
DT   07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2001, sequence version 1.
DT   11-JUL-2006, entry version 29.
DE   MANSC domain-containing protein 1 precursor.
GN   Name=Mansc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

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RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Cecum, Colon, and Medulla oblongata;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam H.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477992; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Contains 1 MANSC domain.
CC   ---------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
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CC   ---------------------------------------------------------------------------
DR   EMBL; AK018660; BAB31329.1; -; mRNA.
DR   EMBL; AK018635; BAB31319.1; -; mRNA.
DR   EMBL; AK033526; BAC28341.1; -; mRNA.
DR   EMBL; AK033557; BAC28357.1; -; mRNA.
DR   EMBL; AK046837; BAC28892.1; -; mRNA.
DR   EMBL; BC039930; AAH39930.1; -; mRNA.
DR   UniGene; Mm.57648;
DR   Ensembl; ENSMUSG00000032718; Mus musculus.
DR   MGI; MGI:1914979; Manscl.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANSC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Glycoprotein; Membrane; Signal; Transmembrane.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    414       MANSC domain-containing protein 1.
FT                                /FTId=PRO_000021638.
FT   TOPO_DOM     25    369       Extracellular (Potential).
FT   TRANSMEM    370    392       Potential.
FT   TOPO_DOM    393    414       Cytoplasmic (Potential).
FT   DOMAIN       32    116       MANSC.
FT   CARBOHYD    128    128       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    234    234       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    335    335       N-linked (GlcNAc...) (Potential).
FT   CONFLICT     11     13       SLL -> ALV (in Ref. 2).
FT   CONFLICT     56     56       L -> V (in Ref. 2).
FT   CONFLICT     63     63       I -> V (in Ref. 2).
FT   CONFLICT    139    139       F -> S (in Ref. 2).
FT   CONFLICT    170    170       R -> G (in Ref. 2).
FT   CONFLICT    192    192       M -> T (in Ref. 2).
FT   CONFLICT    242    242       E -> A (in Ref. 2).
FT   CONFLICT    275    275       G -> A (in Ref. 2).
SQ   SEQUENCE   414 AA;  44823 MW;  29BB197C916BA8E CRC64;

Query Match             52.7%;  Score 1164.5;  DB 1;  Length 414;
Best Local Similarity   59.9%;  Pred. No. 4.3e-68;
Matches  258;  Conservative  37;  Mismatches  119;  Indels  17;  Gaps  6;

Qy     1 MFFGGEGSLTYTLVIICFLTRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
           ||||| ||||||||||| |:|:::||||||:|||||||||||||||||||||||:::||
Db     1 MLFRGT-SLAYSLLVISFLTPRSSAQNCLTKSLEDVVIDIQSSLSKGIRGNEPIHLATQ 59

Qy    61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
           |||| |||||||||||||||||||||||| |||||||||||| :||||||||||||:|:||
Db    60 EDCIGACCSTKDIAGDKACNLMIFDTRKTDRQPNCYLFFCPSDACPLKPAKGLVTYRLI 119

Qy   121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
           ||||||||||| :|||| ||||||| ||||| :|:: || |:||| ||::|: ||| |
Db   120 RDFPLTSANSSLQQLTQGEFILLDHSSPGATPGFRTPAGYPKPTGLSWSDRSSLKSTAPL 179

Qy   181 HLEKLFKMDRASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTSA 240
           |||:|| :||:| | ::| ||  |:||||| ::|||:|||||||||||| ||||:||||
Db   180 HLRKHIKADETSMQL--PEEKSHSQSLQLPSELKMAHLLPKTVPTPPTTVAVAPLRNVSA 237

Qy   241 TPKPATLLPTNASVTPSGTSGQLQPLATTAPPVTTVTSQPPTLISTVFTRAAATLQAMATT 300
           ||| ||| ||||| :|||:|:||| :|:| ||| |:| || |||| |::|     :
Db   238 TLKPELL-TSISVTAKTLKQKE-ATTASPVTTVTSKLPGVPGSTSFT-----PVVTHQ 289

Qy   301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
           |::|| |||| :|||| |||:|: ::||| |:||| || :::|||| || ||:||||| :
Db   290 AALTNTFQAHTDSKGILETMPFQGGSTLIT------SDPRHGKSSTSESSITNKTASWEDR 343

Qy   361 EASPGSSGSVPENQYGLPFEKWILLISLLFGVLFIVIGLVLLGRILSESLRRKRYSRL 420
           |||| ||:| :| |:||| ||||||||||||||||||||||||:|:::||||||||||
Db   344 RVSVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVIGLVLLGRMLVEALRRKRYSRL 403

Qy   421 DYLINGIYVDI 431
           |||||||||||
Db   404 DYLINGIYVDI 414
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RESULT 7
Q52K78_CHICK

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ID   Q5ZKY8_CHICK    PRELIMINARY;    PRT;    449 AA.
AC   Q5ZKY8;
DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   04-APR-2006, entry version 7.
DE   Hypothetical protein.
GN   ORFNames=RCJMB04_8k11;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CB; TISSUE=Bursa;
RA   Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA   Piedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA   Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT   "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT   genefunction analysis.";
RL   Genome Biol. 6:R6-R6(2005).
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AJ719946; CAG31605.1; -; mRNA.
DR   UniGene; Gga.22562; -.
DR   InterPro; IPR011106; MANSC_N.
DR   Pfam; PF07502; MANEC; 1.
DR   PROSITE; PS50986; MANSC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   449 AA;   47885 MW;   972B3AEAAA1D611E CRC64;

Query Match            23.6%;    Score 522;    DB 2;    Length 449;
Best Local Similarity  31.2%;    Pred. No. 7.4e-26;
Matches  149;   Conservative  74;   Mismatches  157;   Indels  98;   Gaps  16;

Qy     16 ICFLTLRL-----SASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCST 70
              :  ||| |      :|||||:|::||:|:||| :::|||||  || |:  ||::||| 
Db      8 LCLLAVSCAMPAPSRGQCAAQRMDNAIIDINLSLPMGIRGARPVHVPTPEACIHACCLG 67

Qy     71 KNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAXGLMSYRII---------- 120
           : :||| |||||: |:  ||||||||:|||||  ||| :|||| :||
Db     68 EKLSGGGKKCNLVIFDAQRASTQPNCYLFHCPSTEACPMKPAMGLVSYXKIAQDTHALEDTS 127

Qy    121 --TDFPSLTRNLP-----------SQELPQEDSLLHGQFSQAVTPLAHH--HTDY 160
             :|| :   :||            :||| :||| :|::  :||:     : :|
Db    128 FKNEDFNSNELSVPSDAGAFISQSQASHQSHTTALQQSVFH-QASELVNHMAKGHVDNTEF 186

Qy    161 SKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLP 220
             : |:  | :|   :  :   |  | ||  :|    :|  :   :|.| :|::|
Db    187 HR------------VFPESQRADSPKSLDPLPRQKVINPPPNISYTVQTG---------- 224

Qy    221 ENVSALPATV-AVASPHTTSATPKPAT--LLPTNASVTPSGTSQPQLATTAPPVTTVT 275
           :|:||| :|  ||:||:| |: ::| |    :|:  |::    |:       |||: |
Db    225 -NPSALFLTTESSVSSPSSTTVTPLPKSTVRLKPHTTSLLTGG------TGPSTVTRT 275

Qy    276 SQPPTTLISTVFTRA--AATLQAMATTAVLTT-TFQAPTDSKGSLETIPFTEISNLTLN 331
              : :|::  :  :    ||:|| ||:| :|  | : | |:: |    :|: ::  :| 
Db    276 ---TTFMLTAIARAEPGIPTAKIAARTRVFLSSLITSASTSTAKWVTSNPVTATSSAGLR 331

Qy    332 TGNV-YNPTALSMSNVBSSTMNKTASWEGREASP---------GSSSQGSVPENQYG 378
           | :   |:| :|::   :  | ::::|   :||           || :|:::  :|
Db    332 TSSIPPEPTAVSASYTSHVTLVSSSSFALSTSAPPMASLNNHKDYDPSDSEGTPSENVQG 391

Qy    379 LP-----FEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI 431
           |       :||:|:|::|||::|:|: |:  |    ||:||||:  |:|||||:| |:
Db    392 RKGFVQLEDKSRLVAALLFGVIFLLLVIALTGKKMWHESLRRKRQYTRLDYLINGMYADV 449
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AC   Q8K0I0;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Mansc1 protein (Fragment).
GN   Name=Mansc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Director MGC Project;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; BC031372; AAH31372.1; -; mRNA.
DR   Ensembl; ENSMUSG00000032718; Mus musculus.
DR   MGI; MGI:1914979; Mansc1.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
FT   NON_TER       1      1
SQ   SEQUENCE   194 AA;   20701 MW;   11C1F299E1FB3C44 CRC64;

Query Match            22.7%;    Score 503;    DB 2;    Length 194;
Best Local Similarity  59.5%;    Pred. No. 4.4e-25;
Matches  122;   Conservative  13;   Mismatches  56;   Indels  14;   Gaps  4;

Qy    227 PATVAVASPHTTSAIPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTV 286
          | |||| :  ||:|  ||| | | ::|||: | ::|:  |:|:|||||||  ||  :|::
Db      4 PTTVAVAPLRNVSATLKPALLL-TSISVTAKTLKQKE-ATTASPVTTVTSKLPAVPGSTS 61

Qy    287 FTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNV 346
          ||       ::  ||:| ||||:|||||::|| |||  ||||           :|:
Db     62 FT-------PVVTHQAALTNFQAHTDSKGILETMPFQGGSTLT-----SDPRHGKSSTS 109

Qy    347 ESSTMNKTASWEGREBASPSGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVLLGR 406
          |||::|||||||:|||  || : ::|  ::::| | |||||||| ||:||:|||:||||
Db    110 ESSITNKTASWEDRRVVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVLLGR 169

Qy    407 ILSESLRRKRYSRLDYLINGIYVDI 431
           : |:||||||||||||||||||||
Db    170 MLVEALRRKRYSRLDYLINGIYVDI 194
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RESULT 8
Q8K0I0_MOUSE
ID   Q8K0I0_MOUSE   PRELIMINARY;   PRT;   194 AA.

RESULT 9
Q8VCP2_MOUSE
ID   Q8VCP2_MOUSE   PRELIMINARY;   PRT;   392 AA.
AC   Q8VCP2;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   1810055G02Rik protein.
GN   Name=1810055G02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---
DR   EMBL; BC019471; AAH19471.1; -; mRNA.
DR   Ensembl; ENSMUSG00000035372; Mus musculus.
DR   MGI; MGI:1919306; 1810055G02Rik.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
SQ   SEQUENCE   392 AA; 41081 MW; 1D79796C791211FA CRC64;

Query Match   8.9%; Score 197.5; DB 2; Length 392;
Best Local Similarity 26.5%; Pred. No. 0.00013;
  Matches   89; Conservative   37; Mismatches 115; Indels   95; Gaps 14;

Qy   156 HHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQF------ 209
          :|||| ||:||||||||::||||:||:|::|||||| :::|||:: ||::||||
Db   88 HGTNTSTPT------------TREGTTDRV------TSRTLAAPTSSGPSSAEQTRPTTIA 130

Qy   210 ---SSDQEIAHLLPENVSALPAT--VAVASPHTT------------------------VTSQPPTTLISTVFTRAAAT 293
             ::|| ||||||||||:|||| ||||:||| ::|||| |:|:|| |
Db   131 GLPSLSTPHAEVPRTNASVSPRTAMAATVAPHTATLAAGTVNTSDPHTRTPSPAKSTPTD 190

Qy   252 -ASVTPSGTSQOPQLATTAPPVTT------------------VTSQPPTTLISTVFTRAAAT 293
           :||:|:||: :|:||| ::|||| |:|:|| |
Db   191 TSSKNPIFTSGAQIGGTTVQLTTDQPVHSTAGRSALPSNATLEPTTTQVQTK-EPSAST 249

Qy   294 LQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVBSSTMNK 353
          ||:|| |: |:| :| :| ::: ::| ::|: :|
Db   250 VPRARATSLSPDVDVISPTTQPS--PTLP-----TQGTGG--PGTLLTTEQVGTKTTSG 298

RESULT 10
Q9H2K4_HUMAN
ID   Q9H2K4_HUMAN   PRELIMINARY;   PRT;   449 AA.
AC   Q9H2K4;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   13-JUN-2006, entry version 18.
DE   DM4E3.
GN   Name=C11orf24;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21295044; PubMed=11401438; DOI=10.1006/geno.2000.6492;
RA   Twells R.C.J., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H.,
RA   Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.;
RT   "The sequence and gene characterization of a 400-kb candidate region
RT   for IDDM4 on chromosome 11q13.";
RL   Genomics 72:231-242(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Twells R.C., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H.,
RA   Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; AF264781; AAG36936.1; -; mRNA.
DR   UniGene; Hs.303025; -.
DR   Ensembl; ENSG00000171067; Homo sapiens.
DR   RZPD-ProtExp; IOH12453; -.
DR   RZPD-ProtExp; W0857; -.
DR   InterPro; IPR001395; Aldo/ket_red.
DR   PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ   SEQUENCE   449 AA; 46101 MW; 11C8BOFCC3BBF921 CRC64;

Query Match   8.9%; Score 197; DB 2; Length 449;
Best Local Similarity 22.2%; Pred. No. 0.00016;
  Matches 117; Conservative   49; Mismatches 166; Indels 196; Gaps 18;

Qy   13 LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVVTSTQEDCINSCCSTKN 72
          |:|: :||:::||| : ::|:|||
Db   5 LVLIWIFSLSLSESHAASNDPRNFVPNKWKGLVKRNASVETVDNKTSEDVTMAAAS--- 61

Qy   73 ISGDKACNLMIFDTRKTARQPNCYLFFCPNERACPLKPAKGLMSYRIITDFPSLTRNLPS 132
          | ::| :| | :||||| PVTLTKG------- 76
Db   62 ---TSAAHLNS 76

Qy   133 QELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEAS 192
               :|||:||: ||:| :   :|:|||
Db   77 MEVTTEDT---------------------SRTDVSEP------ATSGAADGVTSIAPTAVAS 112

Qy   193 AQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATTVAVASPHT-----TSATPKPATL 247
             ::|||:   :|||:|||||||:||||| :|:|||
Db   113 STTAA------SITTAASMTVASSAP-TTAASSTTVASIAPTTAASSMTAASSTPMTL 164

Qy   248 ---LPTNASV--TPS--GTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
             |||:|:| ||| :|:|||||||: ::
Db   165 ALPAPTSTSTGRTPSTTATGHPSLSTALAQVPKSSALPRTATLATLATRA----QTVATT 220

Qy   354 TASWEGREASPGSSSQGSV---------PENQYGLPFE------------KWLLIGSLLFGV 394
          ||| |||:   :|||: ||:| :||||:||||:|
Db   299 TAS------AGPTSRSSGDIKVPTTDSCQPSTGQYLVTIDALTPSLVNRMLLLVVLLVGV 353

Qy   395 LPLVIGLVLLGRILSESLRRKRYSRLDYLINGILYVD 430
          |: | ||: : |: :|::|||:||::|||||||||
Db   354 TLFIAVLVMFALQAYESYKKKDYTQVDYLINGMYAD 389

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Qy      301  A-------------------------------------------------------VLTTTFQAPTDSKG  315
                |
Db      221  ANTSSPMSTRPSPSKIMPSDTAASPVPPMRPAQAGPISQVSVDQPVVNTTNKSTPMPSNT  280

Qy      316  SLETIPFTEISNLTLNTGNVJNPTAL----------------------SMS-NVESSTMNKTASWEG-  359
                 :  |  :      :||:               |||
Db      281  TPEPAPTPTV--VTTTKAQAREPTASPVPVPVPVHTSPIPEMEAMSPTTQPSPMPYTQRAAGP  338

Qy      360  ----------------REASPGSSSQGSVPENOYG--LP----------------FE  382
                           ||:|:  |||     :|:||:|:|:|:|:||||||:|:|
Db      339  GTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQPSTQGQYMVVTTEPLTQAVVD  398

Qy      383  KWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD  430
                |:|||:|: ||      :|         |  :::|:||||||:|:|
Db      399  KTLLLVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD  446
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RESULT 11

ID   Q9D8N1_MOUSE   PRELIMINARY;   PRT;   392 AA.
AC   Q9D8N1;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   04-APR-2006, entry version 21.
DE   10 day old male pancreas cDNA, RIKEN full-length enriched library,
DE   clone:1810055G02 product:hypothetical Threonine-rich region containing
DE   protein, full insert sequence (NOD-derived CD11c +ve dendritic cells
DE   cDNA, RIKEN full-length enriched library, clone:F63010T004
DE   product:hypothetical Threonine-rich region profile containing protein,
DE   full insert sequence).
GN   Name=1810055G02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Henning P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor J., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563 (2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   PubMed=1641073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566 (2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Pancreas;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa H., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira Y., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RA   Adachi J., Aizawa K., Akahira P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Arakawa J., Aizawa M., Carninci P., Akimura T., Arai A., Aono H.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume M., Sano H., Sasaki A.,
RA   Shibata K., Shiraki T., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---
DR   EMBL; AK007868; BAB25319.1; -; mRNA.
DR   EMBL; AK154828; BAE32858.1; -; mRNA.
DR   UniGene; Mm.23780; -.
DR   Ensembl; ENSMUSG00000035372; Mus musculus.
DR   MGI; MGI:1919306; 1810055G02Rik.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
KW   Hypothetical protein.
SQ   SEQUENCE 392 AA; 41095 MW; 6BBA958C73489874 CRC64;

Query Match   8.9%; Score 196.5; DB 2; Length 392;
Best Local Similarity 26.1%; Pred. No. 0.0015;
Matches   88; Conservative   42; Mismatches 110; Indels 110; Gaps 15;

Qy   156 HHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSOFSSDQEI 215

Db   88 HGTNTSTPT-------TREGTTDRV--------TSRTLAVPTSSGPSSAEQTRPTTI 129

Qy   216 AHL-----------LPE-NVSALPAT--VAVASPHTT------------SATPKPATLLPT 250

Db   130 AGLPSLSTPHAEVPRTNASVSPRTAMAATVAPHTATLAAGTVNTSDPHRTPSPAKSTPT 189

Qy   251 N-ASVTPSGTSQOPLATTAPPVTT------------VTSQPPTTLISTVFTRAAA 292

Db   190 DTSSKNPIPTSGAQIOGTTVQLTTDQPVHSTAGRSALSPSNATLEPTTTQVQTK-EPSAS 248

Qy   293 TLQAMATTAVLTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMN 352

Db   249 TVPARATSLSPVDVISPTTQPS--PTLP------TQGTGG--PGTLLTTEQVGTKTTS 297

Qy   353 KTASWEGREASPGSSSQGSV--------PENQYGLPFB--------KWLLIGSLLFG 393

Db   298 GTAS-----AGTSRSSGDIKVPTTDSCQPSTOGQYLVTIDALTPSLVNKMLLLVVLLVG 352

Qy   394 VLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430

Db   353 VTLFIAVLVMFALQAYESYKKKDYTQVDYLINGMYAD 389

RESULT 12
Q96F05_HUMAN
ID   Q96F05_HUMAN   PRELIMINARY;   PRT;   449 AA.
AC   Q96F05;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   13-JUN-2006, entry version 22.
DE   Chromosome 11 open reading frame 24 (C11orf24) (FP2568).
GN   Name=C11orf24; ORFNames=UNQ1872;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skin;
RG   Director MGC Project;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA   Wan D.F., Gu J.R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

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DR   EMBL; BC011765; AAH11765.1; -; mRNA.
DR   EMBL; AY358754; AAQ89114.1; -; mRNA.
DR   EMBL; AF370372; AAQ15208.1; -; mRNA.
DR   Ensembl; ENSG00000171067; Homo sapiens.
DR   HGNC; HGNC:1174; C11orf24.
DR   RZPD-ProtExp; IOH12453; -.
DR   RZPD-ProtExp; W0857; -.
DR   InterPro; IPR001395; Aldo/ket_red.
DR   PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SQ   SEQUENCE   449 AA; 46143 MW; BF984AA360F6C415 CRC64;

Query Match   8.5%; Score 188; DB 2; Length 449;
Best Local Similarity 22.0%; Pred. No. 0.00064;
Matches 116; Conservative 49; Mismatches 167; Indels 196; Gaps 18;

Qy   13 LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCSTKN 72
Db   5 LVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAAS--- 61

Qy   73 ISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPS 132
Db   62 ---PVTLITKG------TSAAHLNS 76

Qy   133 QELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEAS 192
Db   77 MEVTTEDT----------------SRTDVSEP-------ATSGVAADGVTSIAPTAVAS 112

Qy   193 AQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVVASPHT------TSATPKPATL 247
Db   113 STTAA----------SITTAASMTVASSAP-TTAASSTTVASIAPTTAASSMTTAASSTPMTL 164

Qy   248 --LPTNASV-TPS--GTSQQPLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
Db   165 ALPAPTTSTGRTPSTTATGHPSLSTALAQVPKSSALPRTATLATLATRA----QTVATT 220

Qy   301 A--VLTTTFQAPTDSKG 315
Db   221 ANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQAQGPISQVSVDQPVVNTTNKSTPMPSNT 280

Qy   316 SLETIPFTEISNLTLNTGNVYNPTAL------------SMS-NVESSTMNKTASWEG- 359
Db   281 TPEPAPTPTV--VTTKAQAREPTASPVPVPHTSPIPEMEAMSPTTQPSMPYTQRAAGP 338

Qy   360 ------REASPGSSSSQGSVPENQYG--LP------------------FE 382
Db   339 GTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQPSTQGQYMVVTTEPLTQAVVD 398

Qy   383 KWILLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGLYVD 430
Db   399 KTLLLVVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD 446

RESULT 13
Q8WWQ4_HUMAN

ID   Q8WWQ4_HUMAN   PRELIMINARY;   PRT;   1349 AA.
AC   Q8WWQ4;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   30-MAY-2006, entry version 14.
DE   Mucin 5 (Fragment).
GN   Name=MUC5AC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21426417; PubMed=11535137; DOI=10.1042/0264-6021:3580763;
RA   Escande F., Aubert J.-P., Porchet N., Buisine M.P.;
RT   "Human mucin gene MUC5AC: organization of its 5'-region and central
RT   repetitive region.";
RL   Biochem. J. 358:763-772(2001).

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----
DR   EMBL; AJ298318; CAC83675.1; -; Genomic_DNA.
FT   NON_TER   1   1
FT   NON_TER 1349 1349
SQ   SEQUENCE 1349 AA; 135600 MW; 4DC3C1544F1E5EBA CRC64;

Query Match   14;
Best Local Similarity 21.6%; Score 180.5; DB 2; Length 1349;
Matches 88; Conservative 62; Mismatches 174; Indels 83; Gaps 14;

Qy   4 GGEGSLTYTLVI------ICFLTLRLSASQNCLKKSLEDVVID----IQSSLSKGIRGNE 53
Db   517 GGDKE-TYNNIIRSGEKICRRPQEITRLQ-CRAKSHPEVSIEHLGQVVQCSREEGL---- 570

Qy   54 PVYTSTQEDCINSCCSTKNISGD-KACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAK 112
Db   571 -------------------VCRNQDQQGPFKMC--LNYEVR-------VLCCETPKGCPVTSTS 606

Qy   113 GLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQ---------AVTPLAHHHTDY 160
Db   607 VTAPSPLVGEPPAQTQSTSSWQKSRTTTLVTSSITSTTQTSTTSAPTTSTTPASIPSTTS 666

Qy   161 SKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLP 220
Db   667 APTTSTTSAPTTS---------------TTSAPTTSTTSTPQTQTTSSAPTSSTTSAPTT 710

Qy   221 ENVSALPATVAVASP--HTTSATPKPATLLPTNASVTP--------SGTSQPQLATTA 268
Db   711 STISA-PTTSTISAPTTSTTSAPTTNTSAPTTSTTSAPITSTIS 769

Qy   269 PPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNL 328
Db   770 APTTSTTSTPQTQTSTISSPTTSTTPTPQTSTTSSAPTTSTTSAPTTSTTSTPQT 829

Qy   329 TLNTGNVYNPT-ALSMSNVESSTMNKTASWEGREASPGSSSQGSVPE 374
Db   830 SISSAPTSSTTSAPTASTISAPTTSTTSFHTTSTTSPPTSSTTSSSTPQ 876

RESULT 14
Q7YTR7_CABEL
ID   Q7YTR7_CABEL   PRELIMINARY;   PRT;   519 AA.
AC   Q7YTR7;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   04-APR-2006, entry version 17.
DE   Hypothetical protein.
GN   ORFNames=C30H6.11;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.

OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
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CC   ---
DR   EMBL; Z81044; CAE17706.1; -; Genomic_DNA.
DR   UniGene; Cel.30055; -.
DR   Ensembl; C30H6.11; Caenorhabditis elegans.
DR   WormBase; WBGene00007828; C30H6.11.
DR   WormPep; C30H6.11; CE34720.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   SMART; SM00034; CLECT; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   519 AA;   56013 MW;   93C2CFF9EC339D1A CRC64;

Query Match   7.6%; Score 168; DB 2; Length 519;
Best Local Similarity   27.1%; Pred. No. 0.016;
  Matches   58; Conservative   22; Mismatches   96; Indels 38; Gaps 7;

Qy   229 TVAVASPHTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTLLISTVFT 288
              ||| ||||||||||| |||: :| || : || || || :| || || | :|
Db   155 TTTTTTPTTTTTPTTTTTTTTTTTTTTTTTTTTAPTTTTTTTPTTTTTTTPTTTT 214

Qy   289 RAAATLQAMATTAVLTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVES 348
              ||| ||| ||
Db   215 TVPTTTTTTPTTTTTTTTPTTTTTTTTPAT-----TTSVGNNYNDANYYNSNHNE 269

Qy   349 ------STMNKTASWEGREASPGSSSQGSVPEN----QYGLPFE---KWLLIGSL------ 390
                    :: :| :|| : | :
Db   270 AYNYNYTNDNAHYD------NNSNNHNYSENFMRLMLSLPIAFSINFTLNSIYLQHMK 323

Qy   391 --LFGVLFLVIGLVLLGRILSESLRRKRYSRLDY 422
             :| || | :||||||||||||||||||||
Db   324 YDLTSILFNALGTVTL-------LMRKIFCNIQY 350

RESULT 15

RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; BC098053; AAH98053.1; -; mRNA.
DR   UniGene; Rn.16921; -.
KW   Hypothetical protein.
SQ   SEQUENCE   477 AA;   48211 MW;   19F0450C37FC1E4D CRC64;

Query Match   7.5%; Score 165.5; DB 2; Length 477;
Best Local Similarity   27.0%; Pred. No. 0.021;
  Matches   67; Conservative   32; Mismatches 102; Indels 47; Gaps 9;

Qy   223 VSALPATVAVASPHTSATPKPATLLPTNAS---VTPSGTSQPQ---LATTAPPVTTVT 275
              |: || ||||||||||||||| :||| || |:| | |: | |: :| ||
Db   234 VTSAAGTINTSDPHARTLSPAKST--PTNTSSRNPIFTSGAQTQGTTIQVTTDQPVHSTA 291

Qy   276 SQPP-----TTLISTVFTRAAATLQAMATTAVLTTFQA------PTDSKGSLE-TIPF 322
                        ||| |: |: | ||
Db   292 GRPTPSPSNTTLEPNTPKSVASTSSAVVTTTVQQTKEPSASTVPVLPTSMSPEVEATSPT 351

Qy   323 TEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV------- 372
              ||| | || ||||| :| | | | ||
Db   352 TQPSPLLPTQGTGGPGILLTTEQVGTKATAGTAS-----AGPTSRSSGGVKVPTTASCQL 406

Qy   373 -PENQYGLP---------FEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDY 422
                 :|| || ||| | | |||||||||:||:|||||||||||
Db   407 STQGQYLVVTTDPLTPSLVNKMFLLVVLIVGVTLFIAVLMMFALQAYESYKKKDYTQVDY 466

Qy   423 LINGIYVD 430
            |||:|: |
Db   467 LINGMYAD 474

Search completed: September 19, 2007, 18:50:06
Job time : 455 secs